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AY072397 Arabidops
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AP004536 Lotus Jap
AP001575 Oryza sat
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AC006917 Genomic s
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AP00369 Staphyloc
AC06582 Homo sapi
AC055340 Rattus no
AC075685 Oryza sat
AC075971 Sequence
U78866 Arabidopsis
AL021406 Human DNA
AP0011939 Homo sapi
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0 Homo sapi
A06730234FM
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AC092671 Homo sapi
AC098859 Homo sapi
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Lycopersicon pennellii
Eukaryota: Viridiplantaes: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                       Lycopersi
                                   Lycopersi
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Unpublished
2 (bases 1 to 811)
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
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Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B.
Tanksley,S.D.
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AB026658
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AP001939
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                                                                      July 15, 2002, 06:36:27; Search time 1826.14 Seconds (without alignments) 5538.043 Million cell updates/sec
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          GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries
                                                   nucleic search, using sw model
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/protein_id="ARF74287.1"
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/db_xref="di:8272628"
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DLEEAPCVDCLVHVFCEPCALCQEYREIKNRGFDMGIGWQANMDRQSRGVTMPPYHAG
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Tanksley,S.D.
Direct Submission
Submitted (28-APR-2000) Plant Breeding, Cornell University,
Emerson Hall, Ithaca, NY 14653, USA
Location/Qualifiers
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                                                         /organism-"Lycopersicon pennellii"
/db_xref-"taxon:28526"
/nofe="fw2.2; small-fruit"
join(55. .262,365. .574,644. .717)
/gene="ORPX"
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Pred. No. 7.5e-71;
0; Mismatches 0;
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join(55. .262,365. .9gene="ORFX"
/note="LpORFX"
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55. .717
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ilarity 80.4%;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                            Lycopersicon.

1 (bases 1 to 821)
Frary, A., Grandillo, S., van der
Frary, A., Nesbitt, T.Clint., Frary, A., Grandillo, S., van der
Knaap, E., Cong, B., Liu, J., Meller, J., Elber, R., Alpert, K.B. and
Tanksley, S.D.
Franksley, S.D.
Frary, A., a quantitative trait locus key to the evolution of tomato
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Unpublished
2 (bases 1 to 821)
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B.
                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-AER-2000) Plant Breeding, Cornell University, Emerson Hall, Ithaca, NY 14853, USA 1. Cocation/Qualifiers 1. 821
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Lycopersicon esculentum ORFX (ORFX) gene, complete cds
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/db_xref="taxon:4081"
/note="fw2.2; large-fruit"
join(56. .263,365. .574,653. .726)
/gene="OREX"
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llarity 79.4%; Pred. No. 1.4e-68;
Conservative 0; Mismatches 6;
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/gene="ORFX"
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56. .726
                                                                                         Lycopersicon esculentum
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Direct Submission
Submitted (28-APR-
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                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 127892)
van der Hoeven,R.S. and Tanksley,S.D.
Deductions about the number, organization and evolution of genes
the tomato genome based on analysis of large EST collection and
selective genomic sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breeding, Cornell University, 252
                              415
                                                     319
                                                                           475
                                                                                                Gaps
                   356 TGATGTTAGCATGTGGGGGGTAGAGGTGCATTATATTGTTTGCTGGGATTGATGCTGG
                                                               ctagcctatattcctgcttctacaggtctaaaatgagggggcaatatgatctggaagagg
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2 (bases 1 to 127892)

Nesbitt, C.T., van der Hoeven, R.S. and Tanksley, S.D.

Direct Submission

Submitted (20-AUG-2001) Plant Breeding, Cornell Univer
Emerson Hall, Ithaca, NY 14850, USA

1. 127892

1. 127892

Corganism="Lycopersicon esculentum"

Ab_xref="taxon:4081"

Clone="FW2.2 BAC"

V 42761 a 20070 c 20496 g 44565 t
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complete s
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Matches 413; Conserv
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TITLE
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AF411806 61382 bp DNA 11near PLN 07-OCT-2001
Lycopersicon esculentum BAC clone Clemson_Id 207, partial sequence.
AF411806
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
1 (bases 1 to 61382)
van der Hoeven, R.S. and Tanksley, S.D.
Deductions about the number, organization and evolution of gener the tomaco genome based on analysis of large EST collection and unpublished
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                                                                                                                                                                         /organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160.2; DB 8;
Pred. No. 3.2e-32;
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van der Hoeven, R.S. and Tanksley, S.D.
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/note="fragment 2"
a 11562 c 10377 g 19322 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-AUG-2001) Plant Breed
Emerson Hall, Ithaca, NY 14850, USA
Location/Qualifiers
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Best Local Similarity 90.6%;
Matches 193; Conservative
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4

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

DEFINITION

RESULT AY072397

ACCESSION

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Arvolls 725 bp mRNA linear PLN 10-DEC-2001 Arabidopsis thaliana unknown protein (At3g18480; MYF24.19) mRNA, complete cds.
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Litary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagagctt 390
                                                                                                                                                                                                                                                                                                                  271 tcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcaccttgtgtt 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen, M, (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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Submitted (03-DEC-2001) DNA Sequencing and Technology Center.
Stanford University, 855 California Avenue, Palo Alto, CA 94
                                                                                                                                                                                                      154 tgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt
                                         391 aagaaccgtggctttgatatgggaatagggtggcaagctaataggatagacaa 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 AAGCACCGCGGTTACGATATGAGTCTTGGATGGGCGGGGAACGTGGAGAGACAA 463
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/note="This clone is in pBluescript
ecotype: Columbia"
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/db_xref="taxon:3702"
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AY065153.1 GI:17473787
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ABIVDRGSTSCGTAGALYALIAVVTGCACIYSCFYRGKMRAQYNIKGDDCTDCLKHFC
CELCSLTQQYRELKHRGYDMSLGWAGNVERQONQGGVAMGAPVFQGGMTR"
                                                                              PLN 21-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Osoldae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 683)

Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Chan, Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J. Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satcu, M., Skin, Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R., Yamada, K., Direct Submission
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                                                                          AY072397 683 bp mRNA linear PLN 21-JAN-;
Arabidopsis thaliana unknown protein (At1g14870) mRNA, complete
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ecotype: Columbia"
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/organism="Arabidopsis thallana"
/db_xref="taxon:3702"
/chromosome="1"
/clone="RAFL09-28-D02"
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/protein_id="AAL62389.1"
/db_xref="GI:18252925"
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FLI_CDNA.
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Arabidopsis thaliana
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BASE COUNT ORIGIN

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FEATURES

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SM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatorbyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 98942)
Sysotskala V.S., Schwartz, J.R., Yu,G., Toriumi, M., Lenz,C., Liu,S., Lee,J.M., Li,J., Gonzalez,A., Liu,R., Vaysberg,M., Sakano,H., Chin,C., Choi,E., Chiou,J., Altafi,H., Araujo,R., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Dunn,P., Hansen,N., Howny,B., Halzar,L., Khan,S., Kim,C., Palm,C., Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R.,
Federspiel,N.A. and Theologis,A.
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1
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ELTTRGLDFSIGWSCNMQRTWAPPMSQQMMG"

131 c 152 g 225 t
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Arabidopsis thaliana chromosome 1 BAC F24J5 sequence, complete
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                                                                                                                                                                                                                                                                                                                                                 90 gcggtggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactag 149
                                                                                                                                                                                                                                                                                                                                                                                     133 GCAATGGACTTCTGGTCTTTTCAGCTGCAAGACAGTGAAACTGCTTGCCTCACATG 192
                                                                                                                                                                                                                                                                                                                                                                                                                              150 tgtttgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttc 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 atgtgggagtagaggtgcattatattgtttgct---gggactgacaggattgcctagcct 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atattcctgcttctacaggtctaaaatgaggggcaatatgatctggaagaggcaccttg 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 GTTCTCATGCACTTACCGGACCAAGATCCGAAGTTCGGGTTACCGGAGTCTCCAAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagaga 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 TrcGATTGCGTCACTCATTTTTTGTGAATGTTGTGCTCTTTGCCAAGAACACGTGA 432
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                                                                                                                                                                                                                                                                   Length 725;
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                                                                                                                                                                                                                                                                 Score 106.2; DB 8;
Pred. No. 1.2e-17;
0; Mismatches 143;
125. .526
/gene="At3g18480; MYF24.19"
                                        /codon_start=1
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                                                                                                                                                                                                                                                               Query Match 21.6%;
Best Local Similarity 58.4%;
Matches 205; Conservative C
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RRVSNSLKKFTGKPLPLTCTPWKFGSWMGGDRDGNPNYTAKVSLLIFYDLNSKPTGHE
RISLLSRWMAIDLYIREVDSLRFELSTDRCSDRFSRLADKILEKDYMPPNLQKQNEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDVLAVELLØKDARLALTSEHGKPCPGGTLRVVPLFETVNDLRAAGPSIRKLLSIDWY
REPLOKNHOHOEWWGYSDSGKDAGRETAAMELYKAQDEWYAACNEFGKITTLHGR
GGSIGRGGPTYLA JOSQPPGSYMGSILRSTBGGEWYQAKFGIPQTAARQLEYYTTAVL
LATLKPPQPPREEKWRNLMEEISGISCQHTRSTVYENPBFLSYFHEATPQABLGFLNI
GREPPREKSSSGIGHLAAIPWYFAWTOTRFVLPAWLGYGGLGKYSEKGHADDLKEMY
KEWPFFGSTLELIEWARADIPWRHYDEQLYSEKRRGLGTELKEMY
GEWPFFGSTLELIEWARADIPWTHYDEQLYSEKRRGLGTELKELMTTEKYVLVI
SGHEKLLQDNKSLKKLIDSRLPYLNANMLQYEILKRLENDEDNKKLRPATITINGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MTDTTDDIAEEISFQSFEDDCKLLGSLFHDVLQREVGNPFMEKV
ERIRILAQSALNLRMAGIEDTANLLEKQLTSEISKMPLEEALTLARTFTHSLNLMGIA
DTHHSQLLQSGISPDELYKTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLEYNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSESDWEKIDNGSRSGLTSRGSFSSTSOLLLORKLFEBSQVGKTSFOKLLEPPELKRA
SASPYRIVLGEVKELVYRRLLELLIEGLPCEXDPRNSYETSDOLLEPLLLCYBSLO
SSGAPYLADGERLADITRNGSTRGRUVKLDLRQEAARHSEALDAITYLDMGTYSEWD
BEKKLEFLTRELKGRRPLVPQCIKVGPDVKEVLDTRVAABLGSBSLGAYVISAASNA
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TETSLIKTVKSSLGRLSIFGNKGREQSRVIQVLKINLSLCDFYLSTIHGFVVLMVLML
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LERGECLKKQMDILIELKDAFKQKQANGESTQESKEDDSISCTISCEYDSVRGRTEEM
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NPSRTFSAISYLINGSSSKKNGPDGGNKLQISKKKLSHAEKMIKGALTELFKGLNYLK
TYRNLNILAFMNILKKFDKVSIKSEQFKQSFYKVFFSIFDFKTSPFIFQVTGKQILPI
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SLEKGYSFROVOVIPGLLLGFLAILLICPLMFFKSSPKTRIISYIRTYSFPLKVV
MLDFFWADOLCSOYPMIRNIEST JACYY ITGSYATODYEYCKRYKY YRDLAYDYSFLPY
YWRAMOCARRWFDEGETSHLVNLGKYVSAMLAAGTKVAYEKERSLGMLCLUVAMSSVA
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                                                                                                                                                                                     Submitted (17-AUG-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA on Aug 10, 1999 this sequence version replaced gi:5525042. The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1. Location/Qualifiers
Submitted (10-AUG-1999) Plant Gene Expression Center, 800 Buchanan
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join(12650. .13268,13470. .14071,14223. .14352,14653. .1
14855. .15136,15232. .15381,15502. .15654,15754. .16032,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to gb|x90982 phosphoenolpyruvate carboxylase (ppc1) from Solanum tuberosum." /codon_start=1

    98942
    /organism="Arabidopsis thaliana"
    /cultivar="Columbia"

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                                    Street, Albany, CA 94710, USA 4 (bases 1 to 98942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="F24J5"
1121. .6282
/gene="F24J5.1"
                                                                                                        Theologis, A.
Direct Submission
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LSIGDIVKVEKNEFFPADLVLLSSSYEDAICYVETMNIDGETNLKVKGGLEVTSSLRD
EFNFKGFEAFVKCEDPNANLYSFVGTMELKGAKYPLSPQQLLIRDSKLRNTDFIFGAV
EFTGHDVKVLONSTDPPSKRANIEKKMNK IIYLMFFWITMAFIGSVLFGYTRDDLK
DGVMKRWYLRPDSSSIFFDPRRADVAAIYHETTAVMLYSYFPISLYVSIEVYVLOS
IFINQDIHMYVERADSSPIFDPRRAPVAAIYHETTAVMLYSYFPISLYVSIEVYVLOS
IFINQDIHMYVERADKPARRSNLNBELGQVDTILSDKTGTLTCNSMEFIKCSVAGT
AYGRGYTEVBRAMGRRKGGPLVFOSDBNDIDMEYSKRAITERSTVKGFNFRDERIMNG
NWYTETHADVIQKFFRLLAVGHVVLPEVDEDTGKISYERGEFFF
FNRTQTTISYRREDJVSGRYKERYKVLNVLEFNSTRKMSYTVQEEDGKLLLLCKGA
DNVMFERLSKNGREFEEETRDHVNEYADAGLRTLILAYRELDEKEYKVPNERISGAKS
SYSADRESLIEBYTEKIENTLILAYRELDEKEYKVPNERIGDK
SYSADRESLIEBYTEKIENTLILAYRELDEKEYKVFNETIGDK
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d_xref="61:573470"
/translation="WUGGGTKRRRRELQLSKLYTLTCAQACFKQDHSQIGGPGFSRVV
YCNEPDSPEADSRNYSDNYVRTTKYTLATFLPKSLFEQFRRVANFYFLVTGVLAFTPL
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Petunia x hybrida PGPS/D12 (PGPS/D12) mRNA, complete cds.
AF049928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAINIGFACSLLRQDMKQIIINLETPEIQSLEKTGEKDVIAKAŠKENVLSQIINGK
TQCKYSGGNARAALIIOKSLAYALDDIKHIFELEANSGSASVTGCRSSPKQKALYTRL
VKSGNGKTTLAIGDGANDVORLQEADIGYTSGVEGNAMSSDIAARAFRIERLLI
VHGHWCYRRISTMICYFFYKNITFGFTLELYETYTFSSTPAYNDWFLSLYNVFFSSL
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FFITVYGELPSRISTGAYKVFVEALAPSLSYWLITLFVVVATLMPYFIYSALQMSFFP
                                                                                                                                                                                                                                   APYTASSAIVPLLFVIGATMVKEGVEDWRRQKQDNEVNNRKVKVHRGDGSFDAKEWKT
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Butunia x hybrida.

Butunia x hybrida.

Butaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridas; euasteridas I; Solanales; Solanaceae; Petunia.

( pases 1 to 782)

Guyon, V.N., Astwood, J.D., Garner, E.C., Dunker, A.K. and Taylor, L.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 12; Gaps
      a member of PF(00122 E1-E2 ATPases family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 tgtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 tgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 98942;
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6
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0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105.6; DB Pred. No. 8.8e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65187 CATGCACGACTTGCTGCCTCTACACCTT 65160
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58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.5
Best Local Similarity 58.5
Matches 227; Conservative
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SGGEFESDTEDQEEDVETYRENOTSGNON
CEHCGRRKKSSELESESRENGSKLUYGET 1GKSYROBERENGYRRRGSSCSSYSYSLA
SGGEFESDTEDQEEDVETYRENVRSRSEKKYVDQSAKRLKSKREASQMHSRKKRDESST
GYDSRYQKOTFEEDERSONGALFHENDSGNENESGORDLKERLETRYSEDMEIHEFHYNDD
ACTSSONGKLENBEEDTRYHSTRUDSGNENESSOROLKERLETRYSEEDRYSEEMRR
TKYSSQEEGINVLQNFPEVTNNQOPLVEERISKQAGTRTTFEHISESSEIHDIDIRN
TYYSQREDQINQEWBHAGLYSGLGSERKQOPYHIEHWRQTTQSTRTSYSSTRTSDAV
RYTSIQKRSERRLIGGGSTRANGOSSKKROQPYHIEHWRQTTGPRSTSYSTGSYSTGSYS
GYSIQEISHGTSSSGSSLMASRTKLOLVDLYSEEMQGSFTTLIPPSSQLVSRRSGGSYRTG
GYSIQEISHGTSSGSTTANFEHPRAGASVNSQSAGEMGFFSHEDAMGSAHRLEQASE
KYVGEFVKRAKHGYINPETEGRASSNOULKRRDSRSSGGSGAGGSPENDE
TPHFGATEGNAAVGNAIFRKRRGSLMVIADIARLEMGSRAGSPDSSAKPAGRSSSPNE
SYSSATWFSGREHDGSSDDNTKGDKVLPQEAPSLHQVEVGGTSPRSOSEYFGTTKLKQ
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33736. .33824,33936. .34044,34142. .3435,34427. .34552,
34645. .34743,34827. .35018,35097. .35726)
//gene="r2445.6"
/note="Similar to gblAF067820 ATPase II from Homo sapiens
                                                                                                                                                                  join(18096. .18247,18359. .18485,18566. .18694,18799. .18903)
/gene="F24J5.3"
                                                                                                                                                                                                                                                                                                                                                                              /translation="mantaagmspvLapiyspvnTkPinFHFSASFYKPPRPFYKQQN
PISALHRSKTTRVIEVYTRQRNRSFSVFGSLADDSKLNPDEESNDSAEVASIDIKLP
RRSLQVEFTCNSCGERTKRLINRHAYEKGLVFVQCAGCLKHHKLVDNLGLIVEYDFRE
TSKDLGTDHV"
TIYQLYWDFVKDWGLLQHNSNNPWLRNQLMLRQKSIYYFSMYLNLVLRLAWLQTVLHS
SFEHVDYRVTGLFLAALEVIRRGQWNFYRFRIYTDTCVDKIQNICRLENEHLNNAGKF
RAVKTVPLPFREVDEED"
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PAVMEPPVPRPRMVSGSSSLREQVEQQPLSAKSQEETGSVSADSALIQRKLQRNKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPTTAAPPPTTTTPPVSAAQPPASPVTPPPAVTPTSPPAPKVAPVISPATPPPQPPQ
SPPASAPTVSPPPVSPPPAPTSPPPTPASPPPAPASPPPAPASPPPAPASPPPAPVQAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGCEVYSSCDGIRRKNRSFKLRCLEESDECCGGRSCSDDVEAMISFLSEELIDEERKW
NLVSRVKEKKKVGNVRKVSVEGSNSYGNGRVSQRVKKPEGFGRRKEIKEDVKLNERYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MESNSIIWSLLLASALISSFSVNAQGPAASPVTSTTAPPPTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PISLPPAPAPAPAFKKKKKKKKKKKHHHAPAPAPAPIPPSPPVLTDPQDTAPAPSPNTV
TIOX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MFNTYTNSLQWPIRSRNQQDYCSLLPERSESYKLSKAYTSSRCY
CVSSRSSCCCCCSTPSSSSFVKPKVLINPGFVLYGVRQSTLIQWPSFQRRLLVGGGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSERHEGVVSSPSSTILEGGSVSNRMSSTSGNQIVGVDEEEGGNFEFRLPETALTEVP
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WOGPPOLEKKKKNKSNSDPPTPTDHHHHLPKLLNKMHQVLPFFCL"
31249. .35726
/gene="F24J5.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(20404. .24677)
/gene="F24J5.5"
complement(join(20404. .20665,20744. .20871,21079. .21166,
21232. .24677)
/gene="F24J5.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Contains similarity to gi|3329316 cytosine
                                                                                                                                                                                                                                                              /evidence=not_experimental/product="F24J5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region. EST gb|W43306 com/codon_start=1/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F24J5.4"
complement(19258. .19926)
/gene="F24J5.4"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(19258. .19926)
                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD49972.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAD49971.1"
/db_xref="G1:5734706"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD49970.1"
/db_xref="G1:5734705"
                                                                                                                                                                                                                                                                                                                                                                /db_xref-"GI:5734707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"F24J5.4
                                                                                                                             /gene="F24J5.3"
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Matches 171;
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                                                                                       2 (bases 1 to 782)
Guyon,V., Astwood,J.D. and Taylor,L.P.
Direct Submission
Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAD02554.1"
/db_xref="61:4105794"
/dranslation="ASDRPOPPMSSGICDCFODVKGCCLTCWCPCIFFGRIAEVADOG
STSCVVSGTVYLLVYLVTSGFGCCWYSCFYRSKLRNQYYLDEKPCSDLCTHCCCEYCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

    782
/organism="Petunia x hybrida"
/db.xref="taxon:4102"
/Lissue_type="germinating petunia pollen treated with
kaempferol"

              Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia Plant Physiol. 123 (2), 699-710 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacaga 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctatattcctgcttctacaggtctaaaatgaggggggaatatgatctggaagaggcacct 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTCTGATCTCTGTACCCATTGTTGTTGCGAGTACTGCGCATTGTGTCAAGAGTACAGA 387
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HTG: HTGS_PHASE2.
Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1124_H01.
Oryza sativa
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138 c 163 g 238 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 8; Length 782;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                          /product-"PGPS/D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                  163 g
                                                                                                                                                                                                                                                                                                            /gene="PGPS/D12"
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56.6%;
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chromosome 4, clone:LjT15N19, TM0097b,
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Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5666 GITITATGACGIGGITGIGCCCGIGCAICACGIICGGGCAGAICGCGGAGAICGICGACC 5607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 aaggaacaacttcatgtgggagtagaggtgcattatattgtttgctgggactg---acag 253
                           BAC
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, clone:OJ1124_H01
Published Only in Database (2001) In press
2 (bases 1 to 103550)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 103550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90.8; DB 2;
Pred. No. 7.3e-14;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="0J1124_H01"
21927 c 21786 g 30082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lotus japonicus genomic DNA,
complete sequence.
AP004536
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ilarity 59.8%;
Conservative
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(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This as sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%; Score 74.2; DB 2; 59.9%; Pred. No. 1.7e-09; iive 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="P0528B02"
31780 c 31628 g 40874 t
                                                                                                                                                                                                                                                                                                    1. .146017
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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Ecker,J.R.
Direct Submission
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Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S.
Structural Analysis of a Lotus japonicus Genome. I. Sequence
Features and Maping of Fifty-six TAC clones which cover the 5.4 Mb
Regions of the Genome
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitsion
Submitsed (02-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11485 TGGTTGCGGTTGCTTGTACTCATGCTTCTACCGTTCCAAGTTGAGACGCCCAATACATGTT 11544
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                                                                                                                                                                                                                                                     Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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Oryza sativa chromosome 6 clone P0528B02, *** SEQUENCING IN
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0528B02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LjT library"
/note="TM0097b, a part of TAC clone:TM0097"
13546 c 14460 g 24726 t
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lotus japonicus"
/db_xref="taxon:34305"
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Nakamura, Y.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 13269)
Chao, 0. Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Williams, S., Altafi, H., Araujo, R., Conn, L., Conway, A.B.,
Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskala, I., Lenz, C.,
Li, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M.,
Vysotskaia, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACUUB917 132699 bp DNA linear PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence.
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Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
                                                                                                                                                                                                                                                                                                                                              11697 CGATCCTCAATGCGGGCACAGTACAACTTGCAACAGTCGCCTGCTTGGACTGCTGGGTC 11638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 ggtgcattatattgtttgctgggactgacaggattgcctagcctatattcctgcttctac 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 catgtattctgtgaaccttgtgctctttgccaagaatacagagagcttaagaaccgtggc 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 aggictaaaaatgaggggggaatatgaictggaagaggcacctigitgitgatigictigia
                                                                                                                                                   Length 146017;
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100 others
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FLYHQDRESLMEFGNFTDERRAREAESRVRELEEEVRKMSDEIKSRIESFEDCLVDSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF79250.1"
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PFDLSSFGEGNSRIMSKSGGFNLFVRAYFAFLDRRSILFHDGNRHRYNEESSVLIRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIRKMQIIVDSLIRIKPIGENMAIPVINEAMENVYSEIMEIYGWICRRIAEVLPNYHS
KIGKTEADLALKIVAKSMKOGGELKKYFEFCKDLGVSNAQEIPNFVRIPEADVIHLDE
LVRTAMESSEESAERTEIAEEEEEEEEEIETKLSDLITLDHNEEAPASPPRVVVVDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MEFRAYFILYWFOPFRLQCEPVIVLFLCFQMICLKKRORIFLFW
YPEBLHLQOPFLPKMYIFWVLFLRIRWWFDKOVCKSSFTFKOBSLVSKGARGFALGFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASFVSKDESISLGRIFLEANSEEDKCCETLLRKWDQLRPTTQKFVSLVSMVKRIEKEK
ECLIMNLAKAEQEVELVSEQNRELDRENRKFLRQCSAERSHGSNKFNKRKSIKMMSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MQSTCVYRECMRNHAAKLGSYAIDGCREYSQPSTGDLCVACGCH
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20800. 20887,20957. 211088. 21356,21448. 21906,
22006. 22275,22367. 22570,22840. 22917))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(17635. 17815,17901. 18019,18141. 18194,
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/note="hypothetical protein"
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16027.
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                                                                                                                                                 Lubrated (07-MAY-1999) Arabidopsis thaliana Genome Center,
Department of Blology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
4 (bases 1 to 13699)
S Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,
Johnson-Hopson, C., Kham, S., Kim, C., Alfafi, H., Bei, B., Chin, C.,
Chio, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission
L. Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
Department of Blology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
On May 7, 1999 this sequence version replaced gi:4731042.
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FEILYNKDRVIEISARMDPHSLVDLTEDKEVDAEFMTTVKWETETPFEKRMEKYSMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="unknown protein; similar to EST emb|F14394.1"
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                         (bases 1 to 132699)
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                    3 (bases 1 to 137
Ecker, J.R.
Direct Submission
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                                                              AUTHORS
TITLE
JOURNAL
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AUTHORS
REFERENCE
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FEATURES
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http://www.kazusa.or.jp/kasok/ggit-bin/ggd_graph.cgi?c=MOK9
Genes with similarity to proteins in the databases are described
foreduct or 'note' qualifiers. Genes that have no significant
product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail.1.3/,
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGenez (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.ddk/services/NetGenez/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gramlinl.zool.lastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is K2188 and the 3' clone is K2K18.
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DLTAAESS LCEETLDY ENVLAEIEAEK RENKLUGHIPANNLLKTLSERS FSTADLKLEL
OLY VARFLLLTRINLKTAK RENKHAMNIAQKROSSMALLKS OLEY AGNIHPRAMKILL
VSGIHKEAGTSGIFNNILGCIFYQLGCYQASSVLFIKALRSCSSLRNGK PRAKTFSLSO
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EDWDRIKEVFPRKRGWKMLLTSRNEGVGLHADPTCLSFRARIINPKESWKLFERIVPR
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mitsui Pl"
join(893. 1081,1450. 1536,1795. 1911,2007. 2093,
2173. 2343)
/note="gb|AAD55417.1
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join(6625. .7495,7573. .7716,7811. .9501)
/note="gene_id:MOK9.3"
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similar to unknown protein"
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/protein_id="BAB08702.1"
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/note="gb|AAD55417.1
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1. .87459
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   COMMENT
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AGRGGHVNLKHAERARITVNKIPSWVDNLIKKTLLWEDETRKSFLYDGVRLVSILEDY
KLTRKQQEEEKRRYRDQKKMQDLLIKRRESIYGSKPSPRRSNSVRKINGYNGDASVPP
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Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones
DNA Res. 5 (5), 297-308 (1998)
                                                                                                                                                                                                                         DEQDLTLTRKLNEYQTHLRSLQKEKSÖRLNKVLDYVNEVHTLGGVLGVDFGQTVSEVHP
SLAFRPDHEGGSTNLSDPLLDGLHHMIHKLTRERSVRFQKVDKHANNALLLEVTDYHFDA
LAFSPLSVQLKDVAGSTFEKMHLMDTSQEERTKFASVSYVRSSESDTTERTLSSET
IEQVSAEVDCFNKLKASRMKELVMKRTELENLCRLAHIEADTSTSLEKSTALIDSGT
                                                                                                                                                            ELEKECLEIYRRKVDEAANSKAQLHOSLVSIEAEIASLLAALGVFNSHSPMKAKEGSK
SLKEKLAAVRPMLEDLRLQKDERMKQFVDIKAQIEKMSGEISGYSDQLNKTMVGSLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPRRNSAGATNNDIMTTPRSYSSHRQNGYFKEVRRLSTAPLNFVAIPKEDSVSTYTSV
CGSEPDSPLYN"
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                                                                                                                                /translatoldsymbol{	t ion}="MLEIESPTSLCFRTNTTCNALLRELOKIWVDIGESDAEKDRMLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28342. .28470,28565. .28632.28747. .27610,27713. .27814,27911. .286342. .28470,28565. .28632.28747. .28965)
/note="similar to acid phosphatase type 5 emb|CAB63938.1;
similar to EST gb|N96048.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96885 TATAATATTAAAGGAGATGATTGTACTGATTGCCTTAAACATTCTGCTGTGAGCTTTGT 96826
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AB015477 BA000015
AB015477.1 GI:3241925
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   /evidence=not_experimental
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/db_xref="G1:8778212"
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Nakamura, Y.
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Matches 112;
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/db_xref="G1" 97581310.1"
/db_xref="G1" 97581310.1"
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TENKTEKYISDDVGHCRHTYMQIR"
join (40212. 40333, 40410. .40473, 40535. .40654, 40733. .40819,
40898. .41036,41462. .41593,41845. .41871,42139. .42305)
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AB026658 BA000014
AB026658.1 GI:4757414
/translation-"MACVTTILEAALLPSLPAKELQGIGRSPHPSHQIYWAYWAVEDT
LARGSEQNLEIQCTQGGDSIPSDWENLVDEEVEHEKEITEEDFRLMKELEKEMILDGF
LDNDDLLREEMLAGEIEGLIIDDDSQEMTISEQDVPISHRIEEIPATSQSPSNKRNRS
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Direct Submission
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clone:WYF24.
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                                                                                                                                                                                  /pseudo
/evidence-not_experimental
/evidence-not_experimental
38646.38852
/note-"gene_id:MoK9.11
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
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Pred. No. 9.1e-09;
0; Mismatches 79; Indels 3;
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ilarity 61.7%;
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                      CLDDNSLNSVYRILSLSYEDLPTDLKHCFLYLAHFPEDYKIKTRTLYSYWAABGIYDG
LTLIDGGEDLEELVKRNLVYAEKSKNSWRAKLGOMHDWREVCISKRVENRLQIIK
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LPLLRVLDLSSVKFEGGKLPSSIGGLIHLRFLSLHQAVVSHLPSTIRNLKLMLYLNLH
VAIGVPVHPRNLKRENGESLENGENELEGRILESGTGHSSVTDL
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GRAWVCSRGGFPQLAALOISGOSELEEMYPEGSSMPCLRDLIHSCKKLEELPDGLKY
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join(11444. 11494,11595. 11714,11801. 11858,11951. 12051,
12131. 12226,12315. 12408,12642. 12879,13005. 13362)

pir | | 140675
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complement(join(25354. .25513,22811. .26142))
/note="contains similarity to Ac-like transposase gene_id:wox9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWRCSLVFSSPDKIVSVLIHLLPGLVFFTIRWWNPATFAAMHPVGTDRRVSWPYVEDK

KYLFWPLFVPLVYYTLWQVUYELIVWNLRRQRLLRDPEWYNFGYRELSKAEKANNKL

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FLLEVMPRQVIQKEKKKRAEMQPIEEQILHHEAVSHPTENEPKSTET"

Complement (21292. . . 21564)

//octe="gene_id:MOK9.5

unknown protein.
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VPLRWIYYRFKKWHYYLLDFCYYANTIFLVDLLLYPKNEKLFWVCFSFABGPLAWAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPVVKTLARQNLAFCGSSGKIGEDGNGNFLSFIEILADFDPVMI
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RNETEYEEMEAIGKEMVTYCGGLPLAVKVLGGLLANKHTASEWKRVSENIGAQIVGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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similar to unknown protein"
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unknown protein"
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COMMENT

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.16778,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDFSTEISMHFCLLPCAKHVSGLQDKLVLTVFKGDRFALLKQSRISSNTEIWVTKDKI
NSSNNVVWLNLMTLSIPDFPSLFHQLSDISYFIHDMTLILCCDDNQTGVGCIFIARGD
LCKKIQINYVSLGFSQCVYLPSLTSVPLEFRSLQV"
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EKILEIDGTYTQPVLEHVGISTWFGKLILTDHSLYFRALKVSYDFYRKYHLESDLK
OIINEELTGFWGTRLFEDKAVSYOSISLSENYMEFPELKGHFRADVWLTIOQVLYVH
RYINKYKITGLARDBLAKAVLGVMRVQALQELNLTNAMRYENLLPFNLCDQLPGGDL
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                                                                                                                                                                                    EFSSDSWRVIDDIKPPHYMEYFRKCLSLKGNTYWLGIDRRRRPPDLRITLIKFDFGT
EKFGYVPLPPPCQVHGFEASRLSAVGDEKLSLLLVGDSTSNTELWYDSK IGEANVVSW
SKYLSLYPRPWYGFWHGLSFLLDEEKKVLLCCKSKGWMKEEDEDNYYIVGEDTKFILL
NFGVQTIGGYSPIINYVPSLKQJIELAGSKRKRDY"
complement(9242. .10372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKIMGFYRSGSKVWEYDFNSDSWRVLNGILPNWYFDKSYKCVSLKGNTYMLAGAVTDM
GFDLSLQSYDFSTEKFAPVSLPVPSQARSLNGANRLSVVRGEKLALLYRRDKRSKAEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLKIGHRFAIFECASQAFKFIDSPEWPTLAGRGEYVSLNGNLYWTAYNEDTREHFLGS
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slsvgvtghladkkfrrlffdmmvvwevpavasqallsveedatvsleafsriapavp
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LILSVYWDDPPKSSYFCLLTTFIINERWLYVYRALASLESAIFWYLTRCFSREKLMI
ELKYTAPPPNYMEOLYOONGISELEONIODANIYLLKFRALLESLEPOSGKFAIA
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RKHIEKAAKQFQPLTLTKNYRICPINVNLHGTTPSLEVKNEWIELGDRYNEDKDSEIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILETLAEMSTSRELHRSNKSKDTGTLHSSASDMVSQLGSVFGGSSPRSRRETSSLVVG
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16849, .17026,17139, .17476,17622, .17866,17947, .18303,
18385, .18615)
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similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(18942.
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                Submitted (26-AFW-1999) Tashkazu Nakamura, Kazusa UNA Kesenron Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Address for correspondence: Kaso@kazusa.or.jp Address for correspondence: Kaso@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgil-bin/add_graph.ogi?c-WFF24 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brendel, Stanford University, http://www.cbs.dtu.dk/services/NetGene2// and SplicePredictor (Volker Brendel, Stanford University, Http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, https://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

This Sequence is MIEL5 and the 3 clone is K24M9.
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AGSDGFRFVLASQSYVFLCDARSGVPLLKWQHDVEKPCFMDVYSLSELGVRTFESNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKWSKKEQPGVEVVGPVVPLPVLITLHEFHNGCLNSEGEFSPEAEFYNRCNQISKATR
QIANSGRHETTISLDEDRADEMWLNSDSQEEKKTFIAYRPITKTAESDRLQQEVTTFV
SRIRGCKEGDDNAVGRRGLELFDELSPVEMFFENREVNFDKFDMKAMLTDKTFHSQWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MICTESNHQRFSFAGDLGQSDKGTPMEQQPSGPVRRDTTLLDSS
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LNCDIKKSLLCSFPRLTRSNGTGSVALSKREMLRDINHSSQRHGSPRGVPREGVNPSSHMR
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LKHLEVVAHKGSACKSDEVNLLYLPDDEEYKFPRRFNYLELEYLSAHRKGMLAGFLDS
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LRETWSSLPKEILMLAFSNYSEFADVLVDKKKQSLEFLVVPEFPQLPPFLLRNPSSRS
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Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research
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                                  join(24477. .24671,25127. .25201,25295. .25402,25514. .25546,
25816. .25941,26022. .26165,26254. .2664,26744. .26878,
26982. .27200,27291. .27551,27631. .27759,27850. .28318,
28416. .28471)
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TWEEPDDGSSLELHYKDYWLLPTSSIGNCYVEYQGLKPNETADKWIILOGYKHGEVH
VRVTRKVYEIGRRASAGPGTPFNKALLLSNOWKQVMIKFQNLIDDGDLEGLAEALEEL
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Elaeis guineensis microsatellite DNA, clone mEgCIR0230.
AJ271639
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complement(join(29117. .29383,29522. .29641,29726. .29869,
29953. .30004,30121. .30196,30362. .30540,30667. .30708,
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microsatellite; repetitive DNA.
Elaeis guineensis.
Elaeis guineensis.
Elaeis guineensis.
Elaeis guineensis.
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae; Cocceae; Elaeidinae; Elaeis.
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Billotte_N., Risterucci,A.M., Barcelos,E., Amblard,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.6%; Score 71.6; DB 8; Length 88989; Best Local Similarity 57.0%; Pred. No. 9.1e-09; Matches 131; Conservative 0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51388 TCAAACACCGTGGTTTTGACCCCAATATTGGTAATTTTTATTATGAAT 51339
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EGU271639/c
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                                    CDS
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Direct Submission
Submitted (02-FEB-2000) Billotte N., CP, Cirad, BP Avenue Agropolis
F-34032 Montpellier CEDEX 1, 34032, FRANCE
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                                                                                                                                                                                                                                                                                                                                                                  /PCR_conditions="annealing temperature 520C,1.5 mM MgCl2"
/evidence=experimental
/evidence="Forward primer"
/note="Forward primer"
/PCR_conditions="annealing temperature 520C,1.5 mM MgCl2"
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Billotte, N.
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July 15, 2002, 06:36:27 ; Search time 1598.68 Seconds (without alignments) 4153.741 Million cell updates/sec
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BI263865 SET486314
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BM143489 sa454404.
BM17498 sa45404.
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BM18867 sa45607.
BM1887610 sa486607.
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ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: \*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. gb\_est2:\*
gb\_htc:\*
gb\_gss:\*
em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_estba:\*
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BG459056 00829 lea AI179734 EST2266977 AI778763 EST259715 B1922710 EST242614 AI778764 EST229642 B1922710 EST242614 AI778876 EST229643 AI77887 EST229643 AI775220 EST285563 AW092086 EST285563 AW092086 EST285365 AW092086 EST285365 AW175220 EST285365 AW17520 EST285365 AW17520 EST285365 AW178903 EST285003 BW176887 SA174065 BF519667 EST457131 Description A1897534 A1778836 AN778831 A1778763 B1922710 A1778764 A1778837 AW040794 A1775220 AW092086 AW032653 AI773903 BM176887 AW288052 BF519667 Length DB Query Match I 333.7 331.1 331.1 331.1 330.8 330.8 330.8 330.8 330.8 330.8 330.8 330.8 330.8 330.8 330.8 165.6 153 153 153 153 153 151.4 151.4 151.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 150.4 160. 

	BG459056 610 bp mRNA linear EST 19-MAR-2001 00829 leafy spurge Lambda Hybri1AR 2.1 two-hybrid vector cDNA Library Euphorbia esula cDNA clone 35AE 5. similar to ORFX [Ivcobersicon esculentum], accession# ABF74.86, mRNA sequence	BG459056.1 GI:13382381 EST.	leafy spurge. Euphorbia esula Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; Euphorblaceae; Euphorbla.	<pre>1 (bases 1 to 610) Anderson.J.V. and Horvath,D.P. Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)</pre>	Unpublished (2000) Contact: Anderson JV Plants Science Research USDA/ARS, Biosciences Research Lab 1605 Albrecht Blvd., PO Box 5674, Fargo, ND 58105, USA Tel: 701 239 1263 Fax: 701 239 1252 Enall: anderslyfefargo.ars.usda.gov Seg primer: PAD5.		166 a 148 c 146 g 148 t 2 others
RESULT 1 BG459056	LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL COMMENT	FEATURES SOURCE	BASE COUNT

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and 3' ends located at the EcoRI and XhoI sites
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/tlssue_type="carpl"
/tlssue_type="carpl"
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/note="vector: pBlueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon.

1 (bases 1 to 559)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI897534 559 bp mRNA linear EST 18-MAY-2001 EST266977 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED2718, mRNA sequence.
AI897534 IG:5603436
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                             310 CGTAGCGGCGGGAGCAATATATGGAGTACTAGCATGCTTCACAGGATGTGGGATGCTTATA 369
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                                                                                                                                                                                                                                                                                                              330 tgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagaggct 389
                                                               93 gtggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgt 152
                                   Gaps
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                                                                                                                                                                                     390 taagaaccgtggctttgatatgggaatagggtggcaagctaatatggatagacaaagccg
    Length 610;
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                  Indels
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/cultivar="TA496"
/db_xref="taxon:4081"
Score 165.6; DB 10;
Pred. No. 3.1e-39;
0; Mismatches 129;
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1. .559
33.7%;
ilarity 66.0%;
Conservative
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Query Match
Best Local S
Matches 256
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585 bp mRNA linear EST 18-MAY-2001 EST259715 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES6K8, mRNA sequence.
A1778836
EST. 5276877
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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I (bases I to 585)

D'Ascenzo.M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
Contact: CUGI
                                                                                                                                                                                                                                                                                                         154 tgcccttgtatcaccttttggacagatttctgaaatactaaacaaaggaacaacttcatgt 213
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/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cla56k8"
/clone_lib="tomato susceptible, Cornell"
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                 Length 559,
                                                                                              Score 153; DB 9; Length 55
Pred. No. 2e-35;
0; Mismatches 130; Indels
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Lycopersicon.
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         1 (bases 1 to 585)
van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Liang, F.,
van der Hoeven, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato root tissue
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW455311 585 bp mRNA linear EST 18-MAY-2C EST311849 tomato root during/after fruit set, Cornell University Lycopersicon esculentum cDNA clone cLEX10111 5', mRNA sequence. AW453311
                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                   gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagagctt 390
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                           Length 585;
                                                                                                                                           Score 153; DB 9; Length 58
Pred. No. 2e-35;
0; Mismatches 130; Indels
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1. .585
/tissue_type="leaf"
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                                                                                                                                             31.1%;
64.7%;
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                                                                                                                                                                       Matches 244; Conservative
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JOURNAL
COMMENT
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ble, Cornell Lycopersicon esculentum cDNA
                                                                                                                                            /tissue_type="root"
/dev_stage="plants during and after fruit-set"
/dev_stage="plants during and after fruit-set"
/dev_stage="plants during and after fruit-set"
/hote='vector: plantscript sk(-); Site_1: EcoR1; Site_2:
/hots: supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
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D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W. Praser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX10111"
/clone_lib="tomato root during/after fruit:
                                                                                                                                                                                                                                                                                                                                                                                 Score 153; DB 9; Length 585;
Pred. No. 2e-35;
0; Mismatches 130; Indels
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ilarity 64.7%;
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
G.B., Tanksley,S.D. and Giovannoni,J.
Unpublished (2001)
Contact: CUGI
                                                                                                                                                            /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLES - Tomato Pseudomonas Susceptible EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at S' end with EoRI and 3' end with XhoI site"
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                                                                                                                                                                                                                                                                                                                                                                                                                      328 TCATGTTTTTATCGTACAAAATGAGAAACAATACATGTTACCAGAAAGCCCTTGTGGG
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                                        /organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxson:4081"
/clone="clas6c20"
/clone_lib="tomato susceptible, Cornell"
                                                                                                                                                                                                                                                                               Score 153; DB 9; Length 633;
Pred. No. 2.1e-35;
0; Mismatches 130; Indels
                                                                                                                  /tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
            Location/Qualifiers
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A1778764 GI:5276805
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
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larity 64.7%; Pred. No. 2.1e-35;
Conservative 0; Mismatches 130; Indels
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/organism="Lycopersicon esculentum"
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                               /clone="cLEC78G14"
/clone_lib="tomato callus"
                                                                                                                                                                                                                                           /db_xref="taxon:4081"
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Clemson University Genomics Institute
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T20 bp mRNA linear EST 18-MAY-2001 EST259716 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLESGK8, mRNA sequence.
A1778837 I G1:5276878
                         1. (bases 1 to 719)

Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannon,J.J., and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum
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/cultivar="Ril-13 (Rio Grande x Money Maker)"
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/clone="cLES6C20"
/clone=lib="tomato susceptible, Cornell"
/tissue_type="leaf"
/dex_stage="4-week old"
/lab_host="SOLR"
                                                                                                                                                                               100 Jordan Hall, Člemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 2.2e-35;
0; Mismatches 130; Indels
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLES - Tomato Pseudomonas Susceptible EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end With EcoR1 and 3' end with XhoI site" a 93 c 153 g 260 t 1 others
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      Tracheophyta;
                                                                                                   gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagagctt 390
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Embryophyta; Tracheopedons; core eudicots;
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  Eúkaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLE56K8"
/clone_lib="tomato susceptible, Cornell"
/tissue_type="leaf"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 2.2e-35;
0; Mismatches 130; Indels
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EST 18-MAY-2001

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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoR1 and 3' end with XhoI site."
85 c 135 g 215 t l others
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/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="clERN4L22"
/clone="type="leaf"
/fssue_type="leaf"
/dev_stage="type="leaf"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum;
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Ascenco,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
                                                                                                                                                   EST256320 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER14L22, mRNA sequence.
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5 prime sequence.
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Pred. No. 6.3e-35;
0; Mismatches 131;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                             620 bp
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Best Local Similarity 64.5%;
Matches 243; Conservative
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451 ggagttaccatgcccc
                       Lycopersicon.
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/organism="Lycoperaicon esculentum"
/cultivar="Rio Grande PtoR"
/db.xref="taxon:4081"
/clone="cLET10H19"
/clone="Lib="tomato mixed elicitor, BTI"
/clone="lib="tomato mixed elicitor, BTI"
/clone="Lib="tomato mixed elicitor, BTI"
/clone="Lib="tomato mixed elicitor, BTI"
/clone="Tomato mixed elicitor, Site_2:
Xhol; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. Ecori site was destroyed during cloning."
                                                                                                                                                                                                                                           1 (bases 1 to 544)
D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujil,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
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EST 18-MAY-2001
                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                   BTI Lycopersicon esculentum cDNA
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 6e-35;
0; Mismatches 131; Indels
linear
                                                                                                                                                                                                                                                                                                                                                 Generation of ESTs from tomato leaf tissue
  mRNA
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
AW040794 544 bp
EST283658 tomato mixed elicitor,
                                        clone cLET10H19, mRNA sequence. AW040794
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                                                                                                                                             Lycopersicon esculentum
                                                                               AW040794.1 GI:5899548
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Local Similarity 64.5%;
les 243; Conservative (
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D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
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BTI Lycopersicon esculentum cDNA
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            tgccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="cLET18G23"
/clone_lib="tomato mixed elicitor,
/tissue_type="ledf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 151.4; DB 9;
Pred. No. 6.3e-35;
0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of ESTs from tomato leaf tissue Unpublished (1999)
                                                                                                                                                                        EST285362 tomato mixed elicitor, clone cLET18G23, mRNA sequence. AN092086
EST28516051777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.8%;
Best Local Similarity 64.5%;
Matches 243; Conservative
                                                                                        462 GGGATAGCAATGGCTCC 478
                                                                       ggagttaccatgcccc 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .624
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                                                                                                                                                                                                                                                                                                                                                   Lycopersicon.
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                                                                                                                                                                                                                                                                       tomato.
                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                   ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                     VERSION
KEYWORDS
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                                                                                                                                                RESULT 1
AW092086
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EST282101 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET1317, mRNA sequence.
AW039653.1 GI:5898407
EST.
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Xhol; cLET - Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisonicotinic
acid, PHH, jasmonic acid, ethylene, fenthion, EIX,
okadalc acid, or systemin prior to tissue harvest. EcoR1
site was destroyed during cloning."

92 c 120 g 203 t lothers
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
  387
                                                                                                        447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgtt 153
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                                                     331 gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagactt
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clemson University
110 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db xref="taxon:4081"
/clone="cLET1317"
/clone_lib="tomato mixed elicitor, BT
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.6%; Score 150.4; DB 9;
64.2%; Pred. No. 1.2e-34;
iive 0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of ESTs from tomato leaf tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                           451 ggagttaccatgccccc 467
                                                                                                                                                                                                                                                                                      (bases 1 to 585)
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Contact: CUGI
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Length 711; Indels 213

us-09-898-659-1.rst

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525 bp mRNA linear EST 18-MAX-2001 EST255003 tomato resistant, Cornell Lycopersicon esculentum cDNA al773903 mRNA sequence.
Al773903 GI:5271944
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Directionally cloned cDNAs inserted into pBlueScript SK(-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /.organism="Lycopersicon esculentum"
/cultivar="R11-12 (355::Pto in Rio Grande x Money Maker)"
/cultivar="R11-12 (355::Pto in Rio Grande x Money Maker)"
/clone="clERRE71"
/clone="clERRE71"
/clone="type="tomato resistant, Cornell"
/dev.stage="type="leaf"
/dev.stage="type="tomato"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 525)
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Frasar, Wenter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Sukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                   274 GGAGTAAATGGGGCATTATATACAATAATATGTGTGTGACTTCTTGTCCATGTATTTAC 333
                                                                                                                                                                                                                                                                                                                                                           tcctgcttctacaggtctaaaatgaggggcaatatgatctggaagaggcaccttgtgtt 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aagaaccgtggctttgatatgggaatagggtggcaagctaatatggatagacaaagccgg 450
                                                                                        94 tggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgtt 153
                                                                                                                                                                                                                                                                                                                                                                                                     334 TCTTGTTTTTATCGTAACAAATGAGACAACAATATTTGTTGAAAAAAAGTCCTTGTGGA 393
                                                                                                               154 tgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagagtt
                                                                                                                                                                                                  454 AAAAATCAAGGAGTTGATATGTCAATTGGATGGCATGGAAATGTGGAGAGACAAAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                            0; Mismatches 140;
Score 149; DB 10;
Pred. No. 3.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 GGTGTGATCATCCACCAACAGTTGAAGG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggagttaccatgccccttatcatgcagg 479
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1. .525
30.3%;
63.2%;
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prime sequence.
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                       Similarity
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                       Best_Local Simi
Matches 246;
    Query Match
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AUTHORS
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/tissue_type="callus"
/dev_stage="25-40 days old"
/lab.host="xil.Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/noti="vector: pBluescript SK(-); Site_1: sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
36 a 90 c 144 g 241 t
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
G.B., Tanksley,S.D. and tomato callus tissue (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 17-0CT-2001
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                      271 tcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcaccttgtgtt 330
                                                                                                                                                                                                                                            331 gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagaggctt 390
                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                  391 aagaaccgtggctttgatatgggaatagggtggcaagctaatatggatagacaaagccgg 450
208 TGTCCATGTATTACATTTGGACAAAATTGCTGAAAATTGTCGACAAAGGAACAGTTTCTTGT 267
                                                                                        328 FCATGTTTTTATCGTACANAAATGAGAAACAATACATGTTACCAGAAAGCCCTTGTGGG 387
                                                                388 GACTGTTTGCTTCATTTTTGTTGTGAATGTTGTGCTTTATGCCAAGAACATGGTGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B1922592
711 bp mRNA linear EST 17-EST542496 tomato callus Lycopersicon esculentum cDNA clone cLEC77P22 5' end, mRNA sequence.
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="clEC77P22"
/clone="lib="tomato callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                            ggagttaccatgccccc 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 GGGATAGCAATGGCTCC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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Seg primer: T3.
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marran, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wuylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eudlocts;
Rosidae; eurosids I; Fabales; Fabaceae; Paplilonoideae; Phaseoleae;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                             Length 525;
                                                                                                                               Indels
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Public Soybean EST Project
end with EcoRI and 3' end c 109 g 180 t
                                                                                         Score 148.4; DB 9;
Pred. No. 4.8e-34;
0; Mismatches 131;
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BM176887
BM176887.1 GI:17400105
                                                                                       Query Match 30.2%;
Best Local Similarity 64.2%;
Matches 240; Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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Pred. No. 7.7e-34;
0; Mismatches 134; Indels
                                                                                                                                                                                                                 /organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1074-2313"
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="9-11 day old"
/lab_host="DH10B"
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Search completed: July 15, 2002, 07:56:22 Job time: 4795 sec

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Sequence:

Run on:

Searched:

Database

Result No.

Asparagus asparagi Tobacco plant resi Human gene express S cerevisiae apopt Human immune syste Arabidopsis thalia

Human immune/haema Human immune/haema Human immune/haema Human immune/haema

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                               AAC36743
AAV74759
AAC04289
AAH68527
AAQ49754
AAT03097
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AAV08840
AAH68584
AAZ40821
AAA64336
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09-MAR-1999

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                                                                                                        July 15, 2002, 07:56:27; Search time 177.53 Seconds
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                       1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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990S-0142154.
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99US-0127462.
99US-0128234.
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99US-0129845.
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990S-0159330.
990S-0159638.
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990S-0160761.
990S-0160770.
990S-0160770.
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Matches 217; Conservative
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Pred. No. 3.5e-32;
0; Mismatches 134; Indels
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   99US-0155659.
99US-0156568.
99US-0156569.
99US-0157117.
99US-0157865.
99US-0158029.
99US-0158032.
99US-0158033.
99US-0158039.
99US-0159293.
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ID AAC46412 standard; DNA; 456
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Matches 217; Conservative
   24 - SEP - 1999;
28 - SEP - 1999;
29 - SEP - 1999;
04 - OCT - 1999;
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07 - OCT - 1999;
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99US - 0142803 . 99US - 0142920 . 99US - 0142977 . 99US - 0143542 . 99US - 0144005 . 99US - 0144086 . 99US - 0144325 . 99US - 0144325 .
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990S - 0.145087
990S - 0.145192
990S - 0.145195
990S - 0.145218
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990S - 0.145218
990S - 0.145918
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990S-014743.
990S-0147935.
990S-0148171.
990S-0148319.
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99US-0150566.
99US-0150884.
99US-0151065.
99US-0151066.
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99US-0147204.
99US-0147302.
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99US-0147260.
99US-0147303.
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99US-0149723.
99US-0149929.
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990S-0151438.
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990S-0152363.
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                                                                                                                                            Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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   	imes 	ime
                                                                               This is the nucleotide sequence of DNA encoding LSD1-interacting protein K (see AAW72391) of Arabidopsis thaliana. LSD1 interacting genes (see AAW6735-67) were isolated from a yeast gene expression library constructed in plasmid pUG4-5 using RNA from Arabidopsis leaves infected with Pseudomonas syringae. A two-hybrid system was used with LSD1 short and long open reading frames (see AAW6750-51) as balt. LSD1 (see AAW72366-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Because the inactivation of LSD1 by mutation leads to enhanced disease resistance, LSD1 partner proteins represent novel targets for esistance, LSD1 partner proteins represent novel targets for eninearing plants with enhanced resistance to pathogens. Thus, the invention includes all proteins (see AAW72384-96) that interact with the cell death regulator LSD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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plants which show resistance to cell death caused by pathogens or
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Pred. No. 1.5e-16;
0; Mismatches 154; Indels 3
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                                                  Claim 46; Page 62; 88pp; English
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PR 20-JUL 1999; 9905-0144834

PR 21-JUL 1999; 9905-0144834

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58.2%; Pred. No. 3.7e-10;
ive 0; Mismatches 76;
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Pred. No. 3.7e-10;
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Pred. No. 4.8e-08;
0; Mismatches 61;
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Matches 90; Conservative
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99US-0160989
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99US-0140354

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99US-0138094
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                                                                                         Arabidopsis thaliana
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05-MAR-1999

23-MAR-1999

24-MAR-1999

25-MAR-1999

26-MAR-1999

19-APR-1999

19-APR-1999

19-APR-1999

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23-APR-1999

24-MAY-1999

14-MAY-1999

14-MAY-1999

14-MAY-1999

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14-MAY-1999

16-JUN-1999

10-JUN-1999

10-JUN-1999

11-JUN-1999

11-JUN-1999
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Pred. No. 4e-07;
0; Mismatches 56; Indels 0
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990S - 0151930 . 990S - 0151930 . 990S - 0153768 . 990S - 0153768 . 990S - 0153768 . 990S - 0153758 . 990S - 0154779 . 990S - 0154779 . 990S - 0155486 . 990S - 015929 . 990S - 016098 . 990S - 016098 . 990S - 016098 . 990S - 016098 . 990S - 016136 . 990S - 016132 .
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Local Similarity 60.3%;
nes 85; Conservative
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01. SEP-1999;
07. SEP-1999;
13. SEP-1999;
13. SEP-1999;
16. SEP-1999;
22. SEP-1999;
23. SEP-1999;
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24. SEP-1999;
24. SEP-1999;
26. SEP-1999;
27. SEP-1999;
28. SEP-1999;
29. SEP-1999;
20. CCT-1999;
66. CCT-1999;
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07-0CT-1999

12-0CT-1999

13-0CT-1999

13-0CT-1999

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Matches
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ID AAC3
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23.-UUN-1999; 99US-0140334.

R 23.-UUN-1999; 99US-0140334.

R 24.-UUN-1999; 99US-01100334.

R 22.-UUN-1999; 99US-01100334.

R 32.-UUN-1999; 99US-01100334.

R 01.-UUL-1999; 99US-0112036.

R 13.-UUL-1999; 99US-0112184.

R 13.-UUL-1999; 99US-0112187.

R 13.-UUL-1999; 99US-0112187.

R 13.-UUL-1999; 99US-0112187.

R 13.-UUL-1999; 99US-0112187.

R 15.-UUL-1999; 99US-0112187.

R 15.-UUL-1999; 99US-0114066.

R 15.-UUL-1999; 99US-0114184.

R 19.-UUL-1999; 99US-0114184.

R 19.-UUL-1999; 99US-0114184.

R 22.-UUL-1999; 99US-0114184.

R 22.-UUL-1999; 99US-0114184.

R 23.-UUL-1999; 99US-0114314.

R 23.-UUL-1999; 99US-0114318.

R 24.-UUL-1999; 99US-0114314.

R 25.-UUL-1999; 99US-0114312.

R 25.-UUL-1999; 99US-0114313.

R 25.-UUL-1999; 99US-0114313.

R 25.-UUL-1999; 99US-0114313.

R 25.-UUL-1999; 99US-0114313.

R 25.-UUL-1999; 99US-0114313.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.4; DB 21;
Pred. No. 4.1e-07;
0; Mismatches 56;
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|| | | | | | | | 578
attcgagaacaaagcagtggt 598
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60.3%;
990S - 0151438
990S - 0151363
990S - 0152363
990S - 0153070
990S - 0154018
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990S - 0154018
990S - 0155139
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990S - 015931
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990S - 016136
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Best Local Similarity 60.3
Matches 85; Conservative
31-AUG-1999, 01-SEP-1999, 10-SEP-1999, 113-SEP-1999, 115-SEP-1999, 115-SEP-1999, 115-SEP-1999, 115-SEP-1999, 115-SEP-1999, 22-SEP-1999, 23-SEP-1999, 23-SEP-1999, 114-OCT-1999, 114-OCT-
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990S-0140353. 990S-0140695. 990S-0140691. 990S-0141287. 990S-0141287. 990S-0141264. 990S-0142055. 990S-0142059.	990S-0143542 990S-0144085. 990S-0144086. 990S-0144086. 990S-0144331. 990S-0144331. 990S-0144331. 990S-0144333. 990S-0144333. 990S-0144834. 990S-0144834. 990S-0146388. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0147303. 990S-01440888. 990S-0145087. 990S-0145087. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0149338. 990S-014972. 990S-014972. 990S-014972. 990S-014972. 990S-014972.
23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 06-JUL-1999; 06-JUL-1999; 08-JUL-1999; 09-JUL-1999;	13. JUL-1999; 15. JUL-1999; 16. JUL-1999; 16. JUL-1999; 19. JUL-1999; 19. JUL-1999; 19. JUL-1999; 19. JUL-1999; 20. JUL-1999; 20. JUL-1999; 21. JUL-1999; 22. JUL-1999; 22. JUL-1999; 23. JUL-1999; 24. JUL-1999; 25. JUL-1999; 27. JUL-1999; 27. JUL-1999; 28. JUL-1999; 29. JUL-1999; 29. JUL-1999; 20. JUL-1999; 20. JUL-1999; 21. JUL-1999; 22. JUL-1999; 23. JUL-1999; 24. JUL-1999; 25. JUL-1999; 26. JUL-1999; 27. JUL-1999; 27. JUL-1999; 28. JUL-1999; 29. JUL-1999; 29. JUL-1999; 20. JUL-1999; 20. JUL-1999; 21. JUL-1999; 22. JUL-1999; 23. JUL-1999; 24. JUL-1999; 25. JUL-1999; 26. JUL-1999; 27. JUL-1999; 28. JUL-1999; 29. JUL-1999; 29. JUL-1999; 29. JUL-1999; 20. JUL-1999; 20. JUL-1999; 20. JUL-1999; 21. JUL-1999; 22. JUL-1999; 23. JUL-1999; 23. JUL-1999; 24. JUL-1999; 25. JUL-1999; 27. JUL-1999; 28. JUL-1999; 29. JUL-1999; 29
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ne expression ion pathway; sequence; ss.	
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Hybridisatio protein iden metabolic pa Arabidopsis EP1033405-A2 06-SEP-2000, 25-FEB-2000;	25 - FEB - 1999   25 - FEB - 1999   26 - MAR - 1999   27 - MAR - 1999   28 - MAR - 1999   28 - APR - 1999   28 - APR - 1999   29 - APR - 1999   20 - APR - 1
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss
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9905 - 0128234
9905 - 0128714
9905 - 0130077
9905 - 0130610
9905 - 0130891
9905 - 0132407
9905 - 0132484
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990S-0139456
990S-0139459
990S-0139459
990S-0139460
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990S-0139750.
990S-0139773.
990S-0139817.
990S-0140353.
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990S-0136392.
990S-0136782.
990S-0137222.
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99US-0123180.
99US-0123548.
99US-0125788.
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99US-0126785.
99US-0127462.
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99US-0138540.
99US-0138847.
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99US-0139452.
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99US-0139492.
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99US-0137724
                                                   Arabidopsis thaliana
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27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
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23-JUN-1999;
23-JUN-1999;
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16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
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         9905-0151303.
99075-0151303.
99075-01513130.
99075-015313070.
99075-01537070.
99075-0154719.
99075-0154719.
99075-0154719.
99075-0154719.
99075-015536.
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99075-0159038.
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990S-0160814
990S-0160818
990S-0160981
990S-0160981
990S-0161405
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990S-0161359
990S-0161359
990S-0161359
990S-0161359
990S-0161950
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30 - AuG - 1999

31 - AuG - 1999

70 - SEP - 1999

71 - SEP - 1999

72 - SEP - 1999

73 - SEP - 1999

74 - SEP - 1999

75 - SEP - 1999

76 - CCT - 1999

77 - CCT - 1999

78 - CCT - 1999

78 - CCT - 1999

79 - CCT - 1999

71 - CCT - 1999
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14 OCT - 1999;
18 OCT - 1999;
18 OCT - 1999;
21 OCT - 1999;
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22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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28-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
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Matches
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Pred. No. 5.4e-05;
0; Mismatches 41;
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   990S - 0.152363 .
990S - 0.152363 .
990S - 0.153758 .
990S - 0.154018 .
990S - 0.154018 .
990S - 0.154039 .
990S - 0.155139 .
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Gaps

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	. 030143	<b>848686644464464688888664466466466666666</b>

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Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 14922.
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                    (first entry)
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Pred. No. 0.0036;
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Matches 133; Conserment
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RR 22 - JUN-1999 9905-0139761.

RR 22 - JUN-1999 9905-0139761.

RR 10 - JUL-1999 9905-0141862.

RR 12 - JUL-1999 9905-0141863.

RR 12 - JUL-1999 9905-0141863.
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Search completed: July 15, 2002, 09:18:48 Job time: 4941 sec us-09-898-659-1.rni

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Query Match 6.9
Best Local Similarity 49.2
Matches 89; Conservative
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US-08-426-509A-5
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Sequence 79,
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Sequence 254
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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PCT-US95-05008-5
US-08-222-616-19
PCT-US95-04228-19
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US-08-045-806-3
US-08-366-051B-3
US-08-446-908-1
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-08-472-028A-9
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US-08-232-463-14
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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length: 2000000000
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ullrich,, Axel
APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
INTEL OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.8; DB 4;
Pred. No. 0.14;
); Mismatches 92;
US-08-460-402-18
US-08-078-311-20
US-08-460-402-20
US-08-460-402-17
US-08-460-402-17
US-08-12-202-3
US-08-184-327A-1
US-08-184-327A-1
US-08-670-707A-38
US-09-037-601-38
US-09-037-601-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-36
US-08-670-707A-501-5
US-08-474-503-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30,742
ER: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: In COMPATILLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08426509A Patent No. 6326469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 2770 base pairs
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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Gaps

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Indels

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0; Gaps

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2348 GCTTTGAGATTTTTTTTTTTTTAAATATCCTGTAACTACAATGATGGTAAAGCCAT 2407
                                                                                2288 AATCCCATCAGGCTGTTATTATGAAGGAATTTGATTGCTTTGCTGCACAGCAGGACCTGT 2347
                                         aacttcatgtgggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
                                                                                                                       264 cctatattcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcacc 323
  92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STAME: California
CONTYER: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4 APR-1994
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 4-ARR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATE: APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-222-616-19/c
; Sequence 19, Application US/08222616
; Patent No. 5635177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
89; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7607 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415/952-9881
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M. REGISTRATION NUMBER:
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APPLICANT: Bennet
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                                                                                                                                                                               2348 GCTTTGAGATTTTTTTTTTTTTTTTAAAATATCCTGTAACTACAATGATGGTGGTAAAGCCAT 2407
                   204 aacttcatgtgggagtagagtgcattatattgtttgctgggactgacaggattgcctag 263
                                                                                                   264 cctatattcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcacc 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood Clty, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Germany
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24 AAPR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8; DB 5;
Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9505008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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EDNESS: unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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; MOLECULE TYPE:
PCT-US95-05008-5
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
PCT-US95-05008-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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6.9%; Score 33.8; DB 1; Length 7607;

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1455 AATCCCATCAGGCTGTTATTATGAAGGAATTTGATTGCTTTGCTGCACAGCAGGACCTGT 1396
                                                                                                                   264 cctatattcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcacc 323
                                                                                                                                                                           324 ttgtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacag 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 aggactetetacaggaceegatatggcateeetggacetatttgtgatgactatatggca 330
    204 aacttcatgtyggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 aggictaaaaigaggggggaataigaictggaagagggacctigigitgaiigiciigta 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.8%; Score 33.6; DB 4; Length 703; Best Local Similarity 56.2%; Pred. No. 0.08; Matches 63; Conservative 0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET 021A
CURRENT APPLICATION NUMBER: 05/074,121
EARLIER PELICATION NUMBER: 60/094,713
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER PELING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: s1g_peptide
LOCATION: 61..213
UNTER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.1
OTHER INFORMATION: seq VCLCGFFCFPCLG/CQ
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: polyA_signal
LOCATION: 675..680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: polyA_site
; LOCATION: 692..703
US-09-247-155-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 61..405
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                                                                                                                                                                             1455 AATCCCATCAGGCTGTTATTATGAAGGAATTTGATTGCTTTGCTGCACAGCAGGACCTGT 1396
                                                                                                                                                  264 cctatattcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcacc 323
                                                                                                                                                                                                                                        324 ttgtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacag 383
                                                                 204 aacttcatgtgggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Geodel, David
APPLICANT: Geodel, David
APPLICANT: Took of James William
APPLICANT: Took william
APPLICANT: Took william
TITLE OF INVENTION: PROFIEN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech 7--
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 0.23;
0; Mismatches 92; Indels 0
                    92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CAPPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
Best Local Similarity 49.2%; Pred. No. 0.23; Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION UNDBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WENGY M. LEE
REGISTRATION NUMBER: 0,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECHONE: 415/25-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application PC/TUS9504228 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.98;
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.9
Best Local Similarity 49.2
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7607 bases
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
PCT-US95-04228-19/c
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31.6; DB 4; Length 731;
Pred. No. 0.39;
0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/998,416
FILING DATE: Z4-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park CITY: Research Triangle Park COUNTRY: USA
                                                                                                                                                                                   Sequence 254, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.4%;
Best Local Similarity 58.5%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                            1037 CTCGG 1033
                                        484 accag 488
                                                                                                                                                              US-08-998-416-254/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 gaaatactaaaacaaaaggaacaacttcatgtgggagtagaagtgcattatattgtttgctg 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 ggactgacaggattgcctagcctatattcctgcttctacaggtctaaaatgaggggcaa 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 gctctttgccaagaatacagagagcttaagaaccgtggctttgatatgggaatagggtgg 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                   Sequence 14, Application US/08232463
Patent No. 5670367
CENERAL INFORMATION:
PAPLICANT: BORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS:
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 6.6%;
Matches 20; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-0299
COMPUTER READABLE FORM:
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                USA
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                 RESULT 6
US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                       CITY:
STATE:
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GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TILE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
CURRENT PAPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1963). (1965)
OTHER INFORMATION: Stop codon (TGA)
PUBLICATION INFORMATION:
AUTHORS: Walley, K. L.
AUTHORS: Tang, S.
AUTHORS: O'Malley, K. L.
TITLE: The rat dopamine D4 receptor: sequence, gene structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(820)
OTHER INFORMATION: 5' flanking sequence to end of exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (445)..(447)
OTHER INFORMATION: Start codon (initiator methionine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (3264)..(3907)
OTHER INFORMATION: Exon 4 and 3' flanking sequence
                          Sequence 1, Application US/08475742 Patent No. 6121015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1). (3907)
OTHER INFORMATION: Rat D4 Gene
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
(3072)..(3263)
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ON: (2300)..(2406)
INFORMATION: exon
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ION: (2500)..(3071)
INFORMATION: exon
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LOCATION: (1)..(3907)
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NAME/KEY: misc_feature
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; JOURNAL: New Biol.
; VOUME: 4
; PAGES: 1-9
; DATE: 1992
US-08-475-742-1
                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 3907
-08-475-742-1
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ö ï APPLICANT: Bradfield, Christopher Alan
APPLICANT: Dolwick, Kristin Marie
APPLICANT: Dolwick, Kristin Marie
APPLICANT: Poland, Alan
TITLE OF INVENTION: Ah Receptor cDNA and Method of
TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 3049 gagagiccigccggiggtagitggigggiticcgcccigggacaagagcigatagaggga 3108 3109 ggggtcccgggagccgaggagggaaggggaagggtccagtttggaagggtgaaaggtgg 3168 331 gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagaggctt 390 391 aagaaccgiggctitgataigggaatagggiggcaagctaataiggatagacaaagccgg 450 271 tcctgcttctacaggtctaaaatgaggggcaatatgatctggaagaggcaccttgtgtt 330 Gaps 6 tecaaeggtaggatataatetaggtetaatgaaacaaeettatgtteeteeteatgt 65 ö 1; Score 31.6; DB 3; Length 3907; Pred. No. 0.92; 0; Mismatches 94; Indels 0; Ouery Match 6.4%; Score 31.4; DB 1; Length 5261; Best Local Similarity 50.2%; Pred. No. 1.3; Matches 103; Conservative 0; Mismatches 101; Indels 1. MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION UMJER: US/08/045,806
FILING DATE: 19930408 E: Tilton, Fallon, Lungmus & Chestnut 100 South Wacker Drive, Suite 960 ATTORNEY/AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9207
TELEPHONE: (312)-456-8000
TELEPHONE: (312)-456-776 Sequence 3, Application US/08045806 Patent No. 5378822 6.48; 5261 base pairs TELEFAX: (312)-456-777 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 88; Conservative ADDRESSEE: Tilton, Fal STREET: 100 South Wack CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: G6666-4002 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di CDS 383..2927 NUCLEIC ACID unknown TOPOLOGY: unknown MOLECULE TYPE: CDNA Query Match Best Local Similarity Matches 88; Conserva GENERAL INFORMATION: CLASSIFICATION: STRANDEDNESS: 11 3169 gg 3170 NAME/KEY: ; US-08-045-806-3 451 gg 452 US-08-045-806-3 LENGTH: ò g à g ò δλ

Op ò g ò

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2501 GTATTACCACAACATTCCAAATGTACAGAGCTGGACTATGGGGGGGTTTTGAACCA 2560
                                                                                                                                                                                       2561 TCCCCATACCCCACTACTT-CTAGTTTAGAAGATTTTGTCACTTGTTTACAACTTCCTGA 2619
                                                                                                                 126 ccctgctaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08446908
Patent No. 5705149
GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Lupton, Stephen D.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mochizuki, Diane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Worsion 5.1a
SOFTWARE: Microsoft Worsion 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,908
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,205
FILING DATE: 12-APR-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-CCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 26-OCT-1987
ATTORNEY/AGENT INFORMATION:
ANDREY ACCORDER THE APPLICATION NUMBER: US 07/213,566
FILING DATE: 26-OCT-1987
ATTORNEY/AGENT INFORMATION:
ANDREY ACCORDER TO A TANDREY ANDREY ANDREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seese, Kathryn A.
REGLESTRATTON NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 587-0430
TELEPRAX: (206) 233-0644
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            2620 AAACCAAAAGCATGGATTAAATCCA 2644
                                                                                                                                                                                                                                                         186 aatactaaacaaaggaacaacttca 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 1607 base pairs
nucleic acid
EDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-446-908-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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APPLICANT: Bradital, Christopher A.
APPLICANT: Bradital, Christopher A.
APPLICANT: Bradital, Christopher A.
APPLICANT: Carver, Lucy A.
TITLE OF INVENTION: Ah Receptor cDNAs and Genetically
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 South Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
2501 GTATTACCACAACATTCCAAATGTACAGGCTGGACTACCCTATGGGGGAGTTTTGAACCA 2560
                                                                                                                                                                                                                                                                                              2441 TACAAATCTGAATGGATTCTATGCCTTATACACAGAACTTTATTCCTGTAATCAGCCT 2500
                                                                                                          66 atctgcccccggcaccaccacggcggcggtggtcaactggtctttgtcactgttttgatga 125
                                                                                                                                                                                                                                                  126 ccctgctaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctga 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: USA
IP: 6060-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISFRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU-9207-CIP
TELECOMMUNICATION INFORMATION:
TELEPAX: (312)-456-8000
TELEPAX: (312)-456-776
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/366,051B
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2620 AAACCAAAAGCATGGATTAAATCCA 2644
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-366-051B-3
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LENGTH: 1607 base pairs
TYPE: nucleic acid
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CITY: Seattle
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US-08-871-161-1/c
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                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-231-205A-1
                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
SPECIAL ACTION US/08231205A
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Lupton, Stephen D.
APPLICANT: Lupton, Stephen D.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
TITLE OF INVENTION: Therewith
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                  Query Match 6.2%; Score 30.6; DB 1; Length 1607; Best Local Similarity 53.8%; Pred. No. 1.3; Matches 63; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macincosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Mcrosoft Word, Version 5.1a
CURRENT APPLICATION DATA:
FILING DATE: 21.APR-1994
CLASSIFICATION: -4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION 1974

PRIOR APPLICATION NUMBER: US 07/957,649

FILING DATE: 06-0CT-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438

FILING DATE: 13-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209

FILING DATE: 07-0CT-1988

PRIOR APPLICATION NUMBER: US 07/1356

FILING DATE: 26-0CT-1987

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                               mat_peptide
624..1010
                                                                   sig_peptide
549..623
                                    549..1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98101
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NAME/KEY:
                                  LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                  ; LOCATION:
US-08-446-908-1
                                                                                                                     NAME/KEY:
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254 gattgcctagcctatattcctgcttctacaggtctaaaatgagggggcaatatgatctgg 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 aagaggcaccttgtgtttgattgtcttgtacatgtattctgtgaaccttgtgctcttt 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.2%; Score 30.6; DB 1; Length 1607; Best Local Similarity 53.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1. Application US/08871161
Patent No. 5665122
GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Lupton, Stephen D.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mochizuki, Diane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive TITLE OF ENVENTION: Therewith NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
FILING DATE: 09-010-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,908
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/231,205
FILING DATE: 21-APP-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunex Corporation
51 University Street
                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTT-SENSE: NO IMMEDIATE SOURCE: CLORE: mull-7 FEATURE: NAME/KEY: Sig_peptide NAME/KEY: Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conservative
                                                                                                                                                                                                                                                                                                                                mat_peptide
624..1010
                                                                                                                                                                                                                                                                sig_peptide
549..623
TYPE: nucleic acid
STRANDEDNESS: single
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129 tgctaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctgaaat 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: POETLER, Jane E.R.
REGISTRATION NUMBER: 02356.0067-00000
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-408-400
TELEPHONE: 202-408-400
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 7917 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGGNT INPORMATION:
NAME: BENT, SLEPHER A.
REGISTRATION NUMBER: 29,768
                    MBER: US/08/167,854
10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 actaaacaaaggaacaacttcatgt 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   984 ATTATCTACAAAATCCACAAGATCT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS ACCURRENT.
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)836-9300
(703)683-4109
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 60.09
Matches 51; Conservative
                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria STATE: VA
                                              FILING DATE: 10
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 gattgcctagcctatattcctgcttctacaggtctaaaatgagggggaatatgatctgg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 aagaggcaccttgtgttgattgtcttgtacatgtattctgtgaaccttgtgctcttt 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 AAAAGCAGCTICCTITGTATCATCACATACATGTTTTCTAAAAAGTTTGGTTCATT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 30.6; DB 2; Length 1607; 53.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08167854
Patent No. 5952487
GENERAL INFORMATION:
APPLICANT: Sapp, Martin
APPLICANT: Cole, Stewart
APPLICANT: Maine
TITLE OF INVENTION: Nadine
TITLE OF INVENTION: HPV42=Use in Diagnosis
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-0CT-1988
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/113,566
FILING DATE: 26-0CT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                      CDNA to mRNA
                                                                                                                                                                                                                                                                                    LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.29
Best Local Similarity 53.89
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
624..1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
549..623
                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549..1013
                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: muIL-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY;
; LOCATION:
US-08-871-161-1
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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STATE:
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| INFORMATION FOR SEQ ID NO: 14:
| SEQUENCE CHARACTERISTICS:
| LANGTH: 718 base pairs |
| LENGTH: 718 base pairs |
| TYPE: nucleic acid |
| STRANDEDNESS: single |
| TOPOLOGY: Linear |
| Topology: Logical |
| Topology: Logi
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Search completed: July 15, 2002, 08:28:01 Job time: 6684 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2002, 06:46:38; Search time 16.72 Seconds (without alignments) 936.756 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-898-659-2 921 1 MYPTVGYNLGLMKQPYVPPH......NMDRQSRGVTMPPYHAGMTR 163

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Sal	Description	hypothetical prote	protein F27J15.18	unknown protein (i	hypothetical prote		_	_	_	hypothetical prote	probable melibiose	tenascin-like prot	subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	protein-tyrosine k	unknown protein, 5	conserved hypothet	protein-tyrosine k	laminin alpha-1 ch				formate dehydrogen	protein-tyrosine k	protein-tyrosine k	protein-tyrosine k	hypothetical prote	laminin alpha-1 ch	xylose kinase xylB
SUMMAKIES	Ω	E96710	G96527	A96562	G96710	E84885	F84788	T04702	D84556	T02853	F64752	A61625	JC5571	A39490	JC5570	JN0711	D96663	F69857	S57845	MMMSA	S40837	C91231	B86078	AC0946	154237	JN0712	JH0771	T16829	S18253	D83994
	DB	7	7	~	~	~	~	7	~	~	7	7	~	٦	~	٦	7	٦	ч	Н	7	~	~	~	~	-	۲.	~	~	7
	Length	160	224	190	174	244	242	447	417	230	460	782	962	696	975	1134	232	156	1136	3084	300	300	300	300	1122	1123	1125	239	3712	498
dF	Query	43.8	39.7		53	7		13		11	2	10	2	6.6	6.6		9.1	9.0	9.0	9.0			•	8.8				9.8		8.5
	Score	403.5	365.5	288	270.5	193	164	123	115	104.5	98.5	95.5	92.5	91	91	87.5	84	2	82.5	a	81	81	81	81	81	81	81	79.5	79.5	78
	Result No.	н	7	٣	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

protein F27J15.18 [inported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Bate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001 C.Speciesion: G96527 R.P.P. Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

RESULT G96527

protein-tyrosine k	latent transformin	laminin alpha-1 ch	surface antigen se	hypothetical prote	cell-fate determin	protein-tyrosine k	hypothetical prote	glucose-1-phosphat	tumor necrosis fac	nodulin-30 - kidne	retrovirus-related	uromodulin precurs	PACE4A - mouse (fr	gene PACE4 protein	MEGF6 protein - ra
\$24066	A55494	S14458	A36385	T34264	A49128	I58388	T34513	B84167	154182	S42879	D44490	A30452	152527	153282	T13954
н (	?	7	~	7	~	٦	7	7	~	7	7	-	7	7	7
1138	1820	3075	439	2195	2471	1124	3507	238	435	220	380	640	932	937	1574
8.4	8.3	8.3	8.2	8.2	8.3	8.1	8.1	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0
77.5	1,6	92	75.5	75.5	75.5	75	75	74	74	73.5	73.5	73.5	73.5	73.5	73.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 E96710 Hypothetical protein F24J5.15 [imported] - Arabidopsis thaliana C;5pecies: Arabidopsis thaliana (mouse-ear crees) C;Decies: Arabidopsis thaliana (mouse-ear crees) C;Accession: E96710 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Denkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A;Atthors: E96710 A;Accession: E96710 A;Accession	Query Match         43.8%; Score 403.5; DB 2; Length 160;           Best Local Similarity 48.5%; Pred. No. 3.9e-31;         3.9e-31;           Matches 80; Conservative 27; Mismatches 41; Indels 17; Gaps 6;           Qy         8 NLGLMKQPYVPPHYVSAPGTTAR-WSTGLCHCFDPANCLYTSVCPCITFGQISEILNK 66           Db         2 NLSSNDQPSQRIKAKDWSTDLCECWMDINSCCLTCWCPVAFGRISEVVDR 53           Qy         67 GTTSCGSRALYCLL-GLTGL-PSLYSCFYRSKMRQCUFEBAPCVDCLVHYFCEPCAL 123           I:        :  :                               Db         54 GSTSCGVSGALYMITFMLTGYGGSSLYSCFYRTKLRAQYNLKERPCCDCCVHFCCEPCAL 113           Qy         124 CQETRELK-NRGFDMGIGWQANMDRQSRGVTMPPYHAGMTR 163               : :  :   :  :  :  :  :  :  :  :  :
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C, Accession: G96710

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Eughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Liu, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Reference number: A86141; Muin:21016719

A; Accession: G96710

A; Accession: G96710

A; Molecule type: DNA

A; Residues: 1-174 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2945010 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: E8488
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K. S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-244 <STO>
A;Cross-references: GB:AE002093; NID:g4895249; PIDN:AAD32834.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005173; NID:q5734717; PIDN:AAD49982.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F24J5.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                       67 -----GTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEP 120
                                                           RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCP---CITFGQISEILNK---- 66
     35 FAPPNYQQANVNLSVGRPWSTGLFDCQADQANAVLTTIVPCVTFGQIAEVMDEGEMTCPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 QPY-----AEQLPQGLWTTGLCDCHEDAHICTYQNVSLRVFCLIFLLVCCLKTRCKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHA-GMTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.4%; Score 270.5; DB 2 37.8%; Pred. No. 1.8e-18; ive 20; Mismatches 61
                                                                                                                                                                                                     ELKNRGFDMGIGW-----QANMDRQS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 37.8% les 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: E84885
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A; Map position: 1
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Best Local Si
Matches 62,
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Caccession: A6556
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roneay, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
ansen, N.F.; Hughes, B.; Huizar, L.
Alature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4,
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                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: GB:AE005173; NID:g7770345; PIDN:AAF69715.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQSRG----VTM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 FDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGLPSLYSCFYRSKM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYPTVGYNLGLMKQP-YVP------PHYVSAPG---TTTARWSTGLCHC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 YVPPHYVSAPGTTTA--RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.3%; Score 288; DB 2; Best Local Similarity 39.9%; Pred. No. 4.2e-20; Matches 59; Conservative 27; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 365.5;
; Pred. No. 2.2e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%;
41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.8
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-190 <S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: F27J15.18
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 PP 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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4

Gaps

21;

70

H.W.; Mayer, K.F.X.; Schue

5

Gaps

8;

Length 447;

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hypothetical protein At2g17780 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84.56 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A; Reference number: A84420; MUID: 20083487
A; Accession: D84556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002093; NID:96598810; PIDN:AAB80787.2; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein L1439.5 [imported] - Leishmania major (strain Friedlin) C;Species: Leishmania major C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 WHADLLDCCSEPCLCLKTLFFPCGTLAKISTVATSRQISSTEVCKNLIVYSLILSC--- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 WHTDLLACCSEPSLCFKTFFFPCGTLAKIATAASNRHISSAEACNELMAYSLILSC---- 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILN----KGTTSCGSRGALYCLLGLTGLP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILN...-KGTTSCGSRGALYCLLGLTGLP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| | |:| | |:| | 382 CCYTCCVRRKLRKTLNITGGFIDDFLSHVMCCCCALVQELREVEIRG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 SLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRG 134
                                                                         A; Molecule type: DNA
A; Residues: 1-447 < CBEV>
A; Cross-references: BMBL:AL031986
A; Experimental source: cultivar Columbia; BAC clone F4B14
B; Experimental source: cultivar Columbia; BAC clone F4B14
B; Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998
A; Reference number: 215418
A; Accession: T09484
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 SLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELK 131
                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-447 <BEW>
A;Cross-references: EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 123; DB 2;
; Pred. No. 0.00045;
13; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 301/2; 340/1; 364/1; 399/3; 431/1
A;Note: F4B14.190; T19K4.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.8%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                       Reference number: 215380
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Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-417 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: DNA
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A;Map position: 2
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T02853
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N.Alternate names: hypothetical protein T19K4.50
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
R;Bevan, M.; Rose, M.; Hompel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pypothetical protein At2g37110 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84788
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Micrman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 PLVPPPAAEEYGWTADGLPVSHGSVIGEPIRRNQWNSGLFTCLGRNDEFCSSDLEVCLLG 100
                                                                                                                                                                                                                                                                                                                   50 SVCPCITFGQISEILNK--GTTS--CGSRGALY----CLLGLTGLPSLYSCFYRSKMRGQ 101
                                                                                                                                                                                                                                                                                                                                                                                                          TTSCGSRGAL---YCLLGLTGLPS---------LYSCFYRSKMRG 100
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           11 LMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK---G 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ARWSTGL--C----HCFDDPANCLVT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 99
                                                                                                                                                                                                           38;
                                                                                                                                               Length 244;
                                                                                                                                            Query Match 21.0%; Score 193; DB 2; Length 24 Best Local Similarity 27.7%; Pred. No. 5.7e-11; Matches 46; Conservative 23; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 KYHLKNAPCDHCMVHCCLHWCALCQEHREMKNHLSDTEASSSTTMD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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; Pred. No. 3.2e-08;
17; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 DMGIGWQANMDRQSRGVTMPPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 HPG----FNAQSTVVVMPPIEQTMGR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%;
28.8%;
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les 60; Conserv
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A;Gene: At2g37110
A;Map position: 2
At2945010
                                                     A; Map position: 2
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Best Local S.
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                       68
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                       A; Gene:
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C; Species: Homo sapiens (man)
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5571
C; Accession: JC5571
J: Blochem. 121, 941-948, 1997
A; Tille: A novel human PACF4 isoform, PACF4 is an active processing protease contain A; Reference number: JC5570; MUID: 97335942
A; Reference number: JC5570; MUID: 97335942
A; Status: nucleic acid sequence not shown
                                                                                                                                                                    tenascin-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Bate: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jan-2000
C;Accession: A61625; S28463
R;Baumgartner, S.; Chiquet-Ehrismann, R.
Mech. Dev. 40, 165-176, 1993
A;Title: Ten(a), a Drosophila gene related to tenascin, shows selective transcript lay. Reference number: A61625; MUID:93264270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: DDBJ:DBJ:DBJ994; NID:q2330550; PIDN:BAA21792.1; PID:q2330551
A; Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of chit is retained intracellularly.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 VPPHYVSAPGTTT-ARWSTGLCHC-----FDDPANCLVTSVCPCITFGQISEILNKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 GICVA-GQCYCKAGWQGEDCGTIDQQVYQCLPGCSEHGTYDLETGQCVCERHWTGPDCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 TSCGSRGALYCLLGLTGL-----PSLYSCFYRSKMRGQYDLEEAPCV------
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A61625
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-782 < BADJ
A; Cross-references: EMBL:X68794
C; Genetics:
A; Gene: ten-a
A; Cross-references: FlyBase:FBgn0004446
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Keywords: tandem repeat
F; 1-62/Domain: signal sequence #status predicted <SIG>F; 63-782/Product: tenascin-like protein #status predicted <MAT>F; 497-524/Domain: EGF homology <EGF>
     Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 95.5; DB 2; 22.3%; Pred. No. 0.32; iive 15; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 22.3%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSRGVTMPPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 -NGRHCTLPGCENGCSR 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-962 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PACE4
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                                168
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                                                                                                                                         A;Accession: A81463
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <PVL>
A;Cross-references: GB:AE001274; NID:93264850; PIDN:AAC24676.1; PID:92266921; GSPDB:GN0C
C;Genetical source: strain MHOM/IL/81/Friedlin
C;Genetical Source: A;Gene: L1439.5
A;Map position: 1
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                       R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-A;Reference number: A81455; MUID:99178987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable meliblose carrier protein yagG - Escherichia coli
N.Alternate names: probable membrane protein yagG
Species: Escherichia coli
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C.Accession: F64752
C.Bate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C.Accession: F64752
B.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617
A.Reference number: A64720; MUID:97426617
A.Status: nucleic acid sequence not shown; translation not shown
A.Nolecule type: DNA
A.Residues: 1-460 <a href="https://doi.org/10.1007/plus.100767">https://doi.org/10.1007/plus.100767</a>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTS----CGSRGALYCL-LGLTG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCPC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 ITFGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: yagG
C;Superfamily: melibiose carrier protein
F;80-96/Domain: transmembrane #status predicted <TMM1>
F;107-123/Domain: transmembrane #status predicted <TMM2>
F;155-171/Domain: transmembrane #status predicted <TMM2>
F;184-200/Domain: transmembrane #status predicted <TMM4>
F;298-314/Domain: transmembrane #status predicted <TMM4>
F;317-333/Domain: transmembrane #status predicted <TMM5>
F;371-387/Domain: transmembrane #status predicted <TMM6>
F;371-387/Domain: transmembrane #status predicted <TMM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||: | ||: ::|
192 CLPCAIAQHQREIMHQG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 CEPCALCQEYRELKNRG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Conservative
C; Accession: A81463; T02853
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Best Local Similarity
Matches 35; Conserv
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E-II

var

E-I form

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A. Cross-references: DDBJ:DB7993; NID:92330548; PIDN:BAA21791.1; PID:92330549
A; Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of var c) ti is retained intracellularly.
C; Genetics:
A; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 14-Jul-1994 #text_change 16-Jul-1999
C; Date: 14-Jul-1994 #sequenc_revision 14-Jul-1994 #text_change 16-Jul-1999
C; Accession: JN0711; S3141; S57847; A48926; 165403
R; Iwama, A.; Hamaguchi, I.; Hashiyama, M.; Murayama, Y.; Yasunaga, K.; Suda, T.
Biochem. Biophys. Res. Commun. 195, 301-309, 1993
A; Title Molecular cloning and characterization of mouse TIE and TEK receptor tyrosin A; Reference number: JN0711; MUID:93371421
A; Residues: JN0711
A; Molecule type: mRNA
A; Residues: 1-1134 < IWA>
A; Residues: 1-1134 < IWA>
A; Residues: Loin Y; Kozak, C.A.; Andus, K.L.
Ssub, T.N.; Oin, Y.; Kozak, C.A.; Andus, K.L.
Submitted to the EMBL Data Library, March 1993
                                                                                                                     C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5570
E;Accession: JC5570
J. Biochem. 121, 941-948, 1997
J. Biochem. 121, 941-948, 1997
A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain A;Reference number: JC5570; MUID:97335942
A;Accession: JC5570
                                                                 subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice
                                                                                              Species: Homo sapiens (man)
Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 IS----EILNKGTTSCGSRGALYCLLGLTGLPSLYSC----FYRSKMR------GQY- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 DLEEAPCVDCLVHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        741 TAARRCRRCHKGCETCSSRAATQCL-----SCRRGFYHHQEMNTCVTLCPAGFYA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.9%; Score 91; DB
Best Local Similarity 23.8%; Pred. No. 1.1;
Matches 44; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 SAPGITTARWSTGLCH-----C---FDDPANCL--
                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-598,'L',600-1134 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: 532690
A; Accession: 533141
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-975 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A
                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTSCGSRGALYCLLGLTGLPSLYSC----FYRSKMR------GQY-DLEEAPCVDCL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682 STPGSANI-LQTSVCHPECGDKGCDGPNADQCLNCVHFSLGSVKTSRKCVSVCPLGYFGD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 IS----EILNKGTTSCGSRGALYCLLGLTGLPSLYSC----FYRSKMR------GQY- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLEEAPCVDCLVHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 TGVCHPECGDKGCDGPNADQCLNCVHFSLGSVKTSRKCVSVCPLGYFGDTAARRCRRCHK 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              739 GCETCSSRAATQCL-----SCRRGFYHHQEMNTCVTLCPAGFYADESQKNCLKC- 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           ----VTSVCPCITFGQIS----EILNK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ARGSCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 VHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                          F;1-62/Domain: signal sequence #status predicted <SIG>
F;63:149/Domain: propeptide #status predicted <PRO>
F;196-434/Domain: subtilisin homology <SBT>
F;938-954/Domain: hydrophobic cluster #status predicted <HCL>
F;205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F;25/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                     Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 91; DB 1; Length 969; 23.8%; Pred. No. 1.1; Live 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                             40; Indels
C; Keywords: glycoprotein; hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                           10.0%; Score 92.5; DB 24.1%; Pred. No. 0.76; iive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 SAPGTTTARWSTGLCH-----C---FDDPANCL-
                                                                                                                                                                                                                                                                                                                                                                                                           34 TGLCH-----C---FDDPANCL----
                                                                                                                                                                                                                                                                                                                                             42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.8 tes 44; Conservative
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 42; Conserv
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Best Local Si
Matches 44;
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13;

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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: pression NCBI backbone (NCBIP:118662)
A;Note: sequence extracted from NCBI backbone (NCBIP:118662)
B;Modes: J128-1835, 1985
A;Title: Bnodothelial-specific gene expression directed by the tie gene promoter in vivo.
A;Reference number: 152613; MUID:95383653
                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Molecule type; mRNA
A; Molecule type; mRNA
A; Residues: 1-598, L', 600-1134 <SA2>
A; Residues: 1-598, L', 610-1134 <SA2>
A; Cross-references: EMBL:X71425; NID:9296610; PIDN:CAA50556.1; PID:9296611
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
B; Korhonen, J.; Partanen, J.; Armstrong, E.; Vaahtokari, A.; Elenius, K.; Jalkanen, M.;
Blood 80, 2548-2555, 1992
A; Title: Enhanced expression of the tie receptor tyrosine kinase in endothelial cells du
A; Reference number: A48926; MUID:93043301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GB:S79346; NID:g1086920
C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type
C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type
C;Superfamily: protein-tyrosine kinase, receptor type tie #status predicted
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1134/Product: protein-tyrosine kinase, receptor type tie #status predicted <MAT>
F:36-105/Domain: EGF homology <EGI>
F:313-253/Domain: EGF homology <EGI>
F:304-342/Domain: EGF homology <EGI>
F:353-456/Domain: Immunoglobulin homology <IM2>
F:353-456/Domain: Immunoglobulin homology <IM2>
A;Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611
S,Sato, T. N.; Qin, Y.; Kozak, C.A.; Audus, K.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 9355-9388, 1993
A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes
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F;841-849/Region: protein kinase ATP-binding motif
F;43-103,370-424/Disulfide bonds: #status predicted
F;81,159,501,592,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;866,883,975/Active site: Lys, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 GCGAGRWGPG---CVKDCPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 GTTTARWSTGLCHCFDDPANCLVTSVC----PCI-----TFGQISEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;447-528/Domain: fibronectin type III repeat homology FN3A>
F;540-629/Domain: fibronectin type III repeat homology FN3B>
F;638-726/Domain: fibronectin type III repeat homology FN3B>
F;757-782/Domain: transmembrane #status predicted TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
                                                                                                                                                                                       A; Reference number: S57845; MUID: 94022374
A; Accession: S57847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 CEPCALCOEY 127
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Search completed: July 15, 2002, 06:48:13 Job time: 95 sec

319 CONGGICDRF 328

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2002, 06:47:53 ; Search time 11.96 Seconds (without alignments) 527.700 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-898-659-2 921 1 MYPTVGYNLGLMKQPYVPPH......NMDRQSRGVTMPPYHAGMTR 163

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P75683 escherichia	P29122 homo sapien	Q06806 mus musculu	Q9nfh9 eurypelma c		P19137 mus musculu	i esch	Q02858 mus musculu	Q00174 drosophila	O70309 mus musculu		homod	homo	3 пото	6 human	3 homo	1 homo	1 nason	P07911 homo sapien	Q63415 rattus norv	mus n		erwir		P15800 rattus norv	P35444 rattus norv	Q60675 mus musculu	Q09702 schizosacch	P00748 homo sapien	_	Н	7942	P14347 epstein-bar
SUMMARIES	ID	YAGG_ECOLI	PAC4_HUMAN	TIE1_MOUSE	HCYB_EURCA	TIEL_BOVIN	LMA1_MOUSE	FDOH_ECOLI	TIE2_MOUSE	LMA_DROME	ITB5_MOUSE	TIE1_HUMAN	CRBH_HUMAN	LMA1_HUMAN	TIE2_HUMAN	ENV_HV2KR	LMA2_HUMAN	TNR3_HUMAN	PO13_NASVI	UROM_HUMAN	PAC4_RAT	PERT_MOUSE	NFX1_HUMAN	HYIN_ERWHE	PRGR_HUMAN	LMB2_RAT	COMP_RAT	LMA2_MOUSE	NRD1_SCHPO	FA12_HUMAN	SORL_CHICK	PURA_ACTAC	٦,	UL49_EBV
	DB	-		-	-	-	-	-		Н	-	-	-	Н	-	-	Н	7	-	-	-	-	-	7	-		-	Н	-	-	Н	7	н,	7
	Query Match Length	460	696	1134	626	1136	3084	300	1122	3712	798	1138	1376	3075	1124	857	3110	435	383	640	937	914	1104	460	933	1801	755	3106	529	615	1592	259	1786	591
æ	Query	10.7	٠	•	•	9.0	•	•	•	9.0	8.4	8.4		8.3	8.1	8.1	٠	•	•	٠	0. 0.	7.9		7.8	•	•	•	٠	٠	٠	7.7	7.7	7.7	7.6
	Score	98	91	87.5	84	82.5		81	81	٠	٠	77.5	7	9	^		74.5		e.	e.	73.5	'n	٠	72	72	7	•	71.5	71	71	~	70.5	70.5	7.0
	Result No.	-	7	e	₹	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q00175 mus musculu Q63449 rattus norv P31696 gallus gall P781869 homo sapten P13508 caenorhabdl Q05793 mus musculu P76055 escherichia P25266 herpetosiph P12336 rattus norv P01874 canis famil Q07327 drosophila Q14202 homo sapten
PRGR_MOUSE PRGR_RAT AGRI_CHICK CLDA_HUMAN GLPI_CAEEL PGBM_MOUSE YDAO_ECOLI MTEI_HERAU GTRZ_RAT MUC_CANFA
923 923 1955 228 1295 3707 311 437 522 450 597
0.000000000000000000000000000000000000
70 70 70 69 5 68 69 68 5 68
00000000000000000000000000000000000000

## ALIGNMENTS

RESULT 1 YAGG_ECOL YAGG_ECOL YAGG_ECOL DDT 01-NO DDT 01-NO DDT 16-NO CC 1 CC DETWE CC DETWE CC DETWE CC DDT 16-NO CC DT 16
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4
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                                                                                                                                                                                                                                                1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCPC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; 015099; 015100; 09UEJJ; 09UEJJ; 09UEJJ; 09UEJ9; 091607; 094469; 091410; 09UEGJ; 09UEJ7; 09UEJ7; 09UEJ9; 09UEGJ; 09UEGJ; 09VEGJ; 09V4G9; 09V4H1; 01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 40, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-) (Subtilisin/kexin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of a second human subtilisin-like protease gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuda Y.;
"Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                         55 ITFGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of novel cDNAs encoding human kexin-like protease
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                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                              Klefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
Barr P.J.,
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Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji
                                                                                                                                                                        Length 460;
                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                               -> N (IN REF. 2).
AB600588E663C6B7 CRC64;
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SEQUENCE, FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ datab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed-1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                                                                                                                                                      DB 1;
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                                                                                                                                                                    Score 98.5; DB 1
Pred. No. 0.014;
                                                                                                                                                                                                           18; Mismatches
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   POTENTIAL.
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DNA Cell Biol. 10:757-769(1991).
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29.3%;
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                                                                                                               460 AA;
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CONSTITUTIVE SECRETORY PARHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PARHWAY, WITH UNIQUE RESTRICTED

DISTRIBUTION IN BOTH WEUROENDCCRINE AND NON-NEUROENDOCRINE TISSUES

CONSTITUTIVE SECRETORY PARHWAY, WITH UNIQUE RESTRICTED

DISTRIBUTION IN BOTH WEUROENDCCRINE AND NON-NEUROENDOCRINE TISSUES

AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENGES MOTIF.

CATALITIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR

PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS,
WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

COFACTOR: PACEAA IS PROBABLY CALCIUM-DEPENDENT.

SUBUNIT: THE PACEAA-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE

RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMMER SIZED COMPLEX
WHERERS MATURE PACEAA-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT

PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.

CHOCKATION: PACEAA-I AND PACEA-AIL ARE SECRETED. PACEAC

IN ENDOPLASMIC RETICULUM. PACEAA-I AND PACEA-II ARE RETAINED

INTRACELLULARLY PROBBALY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-

TERMINALS. PACEAB MIGHT BE SECRETED.

CHOCKATOR AND PACEACE SHOWN HERE),

PACEACA-II, PACEAB MIGHT BE SECRETED.

CHOCKATOR AND DACEACE SHOWN HERE),

PACEACA-II, PACEAB MIGHT BE SECRETED.

CHOCKATOR AND PACEACE SHOWN HERE NOW PACEACH. IN ADDRESS.

PACEACA-II, PACEAB MIGHT BE SECRETED.

CHOCKATOR AND DACEACE SHOWN HERE NOW PACEACH. IN ADDRESS.

PACEACA-II, PACEAB MIGHT NE PROXAVEATURE.

CHOCKATOR AND DATE STORMS PACEACH. IN ADDRESS.

PACEACA-II, PACEAB MIGHT NE PROXAVEATURE.

CHOCKATOR AND DATESTALL AND PACEACH. IN ADDRESS.

PACEACA-II, PACEAB PRODUCTS. BISCORNS. PACEACH. IN ADDRESS.

CHOCKATOR AND PACEACH. IN ADDRESS.

PACEACA-II, PACEAB MIGHT NE PROXAVEATURE.

CHOCKATOR AND DATESTAL AND PACEACH. IN ADDRESS.

PACEACA-II, PACEAB PRODUCES.

CHOCKATOR AND DATESTALLY AND TARTER.
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TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE44 IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLES, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
PLACENTA AND PITUITARY. PACE4E-II IS EXPRESSED IN CEREBELLUM,
MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
A novel human PACE4 isoform, PACE4E is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
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DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease."; J. Biochem. 122:438-452(1997).
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Tsuji A., Matsuda Y.;
"Biosynthetic processing and quaternary interactions of proprotein
convertase SPC4 (PACE4).";
FEBS Lett. 434:155-159(1998).
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MEDLINE-97064242; PubMed-8906861;
Zhong M., Benjannet S., Lazure C., Munzer S., Seldah N.G.;
Ernctional analysis of human PACE4-A and PACE4-C isoforms:
identification of a new PACE4-CS isoform.";
FEBS Lett. 396:31-36(1996).
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN
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                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                           EMBL;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                             103 DLEEAPCVDCLVHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and characterization of mouse TIE and TEK receptor tyrosine kinase genes and their expression in hematopoietic stem
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                      ----VTSVCPCITFGQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIR=BALBAC: TISSUE-Lung;
STRAIR=BALBAC: TISSUE-Lung;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
File-1 and tie-2 define another class of putative receptor tyrosine
Winase genes expressed in early embryonic vascular system.";
Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 30, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRALN=BALBAC; TISSUB=Liver;
MEDLINE-9371421; PubMed-8395828;
Iwama A., Hamaguchi I., Hashiyama M., Murayama Y., Yasunaga K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C; TISSUE=Bone marrow;
Krivsov A.V., Ershler M.A., Visser J.W.M., Belyavsky A.V.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           47; Indels
                                                                                                                                   DB 1; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 195:301-309(1993)
                                                                                                                                                                                                                      SAPGITIARWSIGLCH-----C---FDDPANCL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1134 AA
                                                                                                                                                         ; Pred. No. 0.18
16; Mismatches
                                                                                                                              Score 91;
Pred. No. (
                      JOINED.
JOINED.
JOINED.
BAA21625.1; J
BAA21625.1; J
BAA21625.1; J
BAA21625.1; J
BAA21625.1; J
                                                                                                                                9.9%;
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                                                                                                                                                                           Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
                      EMBL; AB001905; B
EMBL; AB001906; B
EMBL; AB001907; B
EMBL; AB001908; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 PYHAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              831 DCEPG 835
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Q06806;
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us-09-898-659-2.rsp

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                                                                       DOMAIN.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
         tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROSINE-PROTEIN KINASE RECEPTOR TIE-1.
                                             ENDOTHELIAL CELLS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00181; BGF; 2.
SMART; SM00160; FN3; 2.
SMART; SM00409; IG, 1.
SMART; SM00410; IG_11ke; 1.
SMART; SM00110; IG_11ke; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00122; BGF_L; 3.
PROSITE; PS01186; EGF_L; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
                                                                                                                                                                                                                                                                        MGD; MGI:99906; Tiel.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000561; EM_pkinase.
InterPro; IPR001961; FW_III.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig.
InterPro; IPR003600; Ig_HRC.
InterPro; IPR003600; Ig_like.
InterPro; IPR001406; Ig_like.
Pfam; PF00008; EGF; 2.
Pfam; PF00041; fin3; 3.
Pfam; PF00047; ig; 2.
Pfam; PF00047; ig; 2.
Pfam; PF00047; ig; 2.
Pfam; PF00069; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                               EMBL; X80764; CAA56739.1; --
EMBL; X73960; CAA52148.1; --
EMBL; S79346; --; NOT_ANNOTATED_CDS.
HSSP; P11362; 1FGK
                                                                                                                                                                                                                     EMBL; X71425; CAA50556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866
975
1003
81
159
501
592
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CARBOHYD
CARBOHYD
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MOD_RES
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DOMAIN
NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
MEDLINE-20564303; PubMed=10961996;
Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma californicum. Structure and intramolecular evolution of the subunits.";
                                                                                                                                                                                                                                                                                                              212 GCGAGRWGPG---CVKDCPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQE 268
                                                                                                                                                                                                                                                                                                                                                                            64 LNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                      269 QCPGTAGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPDHFGADCRLQCQ 318
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 275:39339-39344(2000).
-!- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                       --TFGQISEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARTHROPOS.

-1- SUBDITI: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-1- SUBCELLUTAR LOCATION: Extracellular.
-1- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGAND (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eurypelma californica (American tarantula).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0187; HAEMCYANIN.
PROSITE; PS00209; HEMCYANIN.1; 1.
PROSITE; PS00210; HEMCYANIN.2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
                                                                                                                           Length 1134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                         Indels
-> L (IN REF. 1).
; 0F212ED6C50ACA0E CRC64;
                                                                                                                                                                                         48;
                                                                                                                           Score 87.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 AA
                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                   26 GTTTARWSTGLCHCFDDPANCLVTSVC----PCI--
                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000896; Hemocyanin.
InterPro; IPR002227; Tyrosinase.
                             1134 AA; 124698 MW;
   ĸ
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                                                                                                                           9.5%;
                                                                                                           Ouery Match
Best Local Similarity 26.2'
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hemocyanin B chain (HcB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 CEPCALCQEY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 CONGGICDRF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY.
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Q9NFH9;
                             SEQUENCE
   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCYB_EURCA
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FN\_III.

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LMA1_MOUSE
P19137;
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DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
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SEQUENCE
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LMA1_MOUSE
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         DORNAMA MARKANA MARKAN
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TISSUE-Endothelial cells;

MEDLINE-94022374; Pubmed-8415706;

Sato T.N., Qin Y., Kozak C.A., Andus K.L.;

"Tie-1 and tie-2 define another class of putative receptor tyrosine
"fine-1 and tie-2 define another class of putative receptor tyrosine
"fine-1 and tie-2 define another class of putative receptor tyrosine
"roc. Natl. Acad. Sci. U.S.A. 90:9355-9358 (1993).

-I- FUNCTION: PROBABLE PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
                                                                                                                                                                                                                                                                                                                                                                            81 IGLIGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIG 140
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

COPPER 1 (BY SIMILARITY).

COPPER 1 (BY SIMILARITY).

COPPER 2 (BY SIMILARITY).

N.LINED (GLCNAC. . .) (POTENTIAL).

N.LINED (GLCNAC. . .) (POTENTIAL).

W; 17E4FB28C91F9974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOTHELIAL CELLS.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-i- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                 Query Match 9.1%; Score 84; DB 1; Length 626; Best Local Similarity 33.8%; Pred. No. 0.57; Matches 26; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1136 AA
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InterPro; IPR000561; EGF-like.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                         71966 MW;
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SVAILHRQDCRGVSLPP 111
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315
626 AA;
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Q06805;
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TIE1_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 GCEAGRWGQDCTKECPGCLHGGVCH--DQDGEC----VCPPGFTGTRCEQACREGRFGQS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLV 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GTTTARWST------CLCHCFDDPANCLVTSVCP------CI--TFGQI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;
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EXTRACELLULAR (POTENTIAL).
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EGF-LIKE 2.
EGF-LIKE 3.
IG-LIKE C2-TYPE DOMAIN 2.
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IG-LIKE C2-TYPE DOMAIN 1.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Laminin alpha-1 chain precursor (Laminin A chain).
LAMAI OR LAMA-1 OR LAMA.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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SWART; SMOO180; FOF; 2.
SWART; SMOO1409; IG; 1.
SWART; SMOO1409; IG; 1.
PROSITE; PSOO167; PROTEIN_KINASE_ATP; 1.
PROSITE; PSOO109; PROTEIN_KINASE_DOM; 1.
PROSITE; PSOO102; EGF_1; 3.
PROSITE; PSO0186; EGF_1; 3.
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InterPro; IPR003599; Ig_
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00008; EGF; 2.
Pfam; PF00041; fi3; 3.
Pfam; PP00047; ig; 2.
Pfam; PP00069; pkinase; 1.
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ProDom; PD003031; Laminin_B;
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                                                                                                                                                                                                                                               EUT. J. BLOCHEM. 177:35-45(1988).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DUBLYNG EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELULAR MATRIX COMPONENTS.
-!- SUBDINIT: LAMININ IS A COMPLEX GIYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISJULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE ALPHA-1 CHAIN IS A SUBDINIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                                                                                                                                                                                                                                                                                                                                                  COMPLONENT: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

SIMILARITY: CONTAINS I LAMININ N-FERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS I LAMININ N-FERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
                                                                                                                                                                              SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89030693; PubMed-3181157;
Deutzmann R., Huber J., Schmetz K.A., Oberbaeumer I., Hartl L.;
"Structural study of long arm fragments of lamini. Evidence for repetitive C-terminal sequences in the A-chain, not present in the B-chains.";
                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89034134; PubMed=3182802;
Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;
"Laminin, a multidomain roctein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the
                                                                                                                            SEQUENCE OF 1-339 FROM N.A.
MEDLINE-88225080; PubMed=3367223;
Hartl L., Oberbaeumer I., Deutzmann R.;
"The N terminus of laminin A chain is homologous to the B chains.";
Eur. J. Blochem. 173:629-635(1988).
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                           J. Biol. Chem. 263:16536-16544(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04064; AAA39410.1; --
EMBL; X07737; CAA30561.1; --
EMBL; X13459; CAA31807.1; --
EMBL; M36775; AAA39406.1; --
FIR; A31771; MAMSA.
HSSP, P02468; 1TLE.
MGD; MGI:99892; Lamal.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001986; Laminin_B.
InterPro; IPR001991; Laminin_G.
Fam; PF00053; laminin_G.
Pfam; PF00053; laminin_G.
Pfam; PF00054; laminin_G.
Pfam; PF00054; laminin_G.
Pfam; PF00054; laminin_Nterm; I.
PRINTS; PR00051; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD002082; LamNT; 1.
                              MCBI_TaxID=10090;
                                                                                                  laminin B chains
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SWART; SW00180; EGF_Lam. 14.

SWART; SW00281; LamB; 2.

SWART; SW00282; LamG; 5.

SWART; SW00136; LamNT; 11.

PROSITE; PS01022; EGF_1; 11.

PROSITE; PS01248; LAMININ_TYPE_EGF; 15.

Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                  LAMININ BEGF-LIKE 1.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
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LAMININ EGF-LIKE 7.
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LAMININ EGF-LIKE 16.
LAMININ G-LIKE 17.
LAMININ G-LIKE 18.
LAMININ G-LIKE 18.
LAMININ G-LIKE 19.
LAMININ 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99069333; PubMed-9852007;
MEDLINE-99069333; PubMed-9852007;
Medit S., Abaibou H., Mandrand-Berthelot M.-A.;
Benoit S., Abaibou H., Mandrand-Berthelot M.-A.;
"Topological analysis of the aerobic membrane-bound formate dehydrogenase of Escherichia coll.";
"J. Bacteriol. 180:6625-6634(1999).
"J. Bacteriol. 180:6
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                     STRAIN=K12; MEDLINE=96099298; PubMed=8522521; MEDLINE=96099298; PubMed=8522521; Mandrand-Berthelot M.-A.; Mandrand-Berthelot M.-A.; Expression and characterization of the Escherichia coli fdo locus and a possible chysiological role for aerobic formate dehydrogenase.";
  beta subunit) (FDH-2 beta subunit) (Aerobic formate dehydrogenase
                                             Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE00046, AAD13455.1; -.
PIR; $40837; $40837.
PIR; $40837; $40837.
ECGENE; ETPX.
ECGENE; ETPR01450; 4Fe4S_ferredoxin.
PRINTS; PR0037; fer4; 1
PRONTS; PR0033; 4FE4SFRDOXIN.
PROSTE; PS00198; 4FE4S_FEREDOXIN; 1.
ELECTION transport; 4Fe-45; Iron-sulfur; Transmembrane; Complete proteome.
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PERIPLASMIC
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93347969; PubMed=8346018;
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01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Formate dehydrogenase-0, iron-sulfur subunit (Formate dehydrogenase-0
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INTERCHAIN (PROBABLE)
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 13;
                                                                                                                                                                    58 TVGNNIGV----YDNPNDLSAKSWTVMRFSEVEQNDKLEWLIRKDGCMHCSD--PGCL-- 109
                                                                                                                                                                                                                                            161 -----TLCVDRVV-VGQEPACVKTCPTGAIHFGTKESMKTLASERVAELKTRGYD 209
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumont D.J., Gradwol G.J., Fong G.-H., Auerbach R., Breitman M.L.;
"The endothelial-specific receptor tyrosine kinase, tek, is a member of a new subfamily of receptors.";
Oncogene 8:1293-1301(1993).
                                                                                                                                                                                                                         96
                                                                                                                                                 -----TGLCHCFDDPANCLVT 49
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY). 950B40FE1A6016E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation (RC)
18-OCT-2001 (TEC. 40, Last annotation (RC)
18-OCT-2001 (Rel. 40, Last annotation (RC)
18-OCT-2001 (RC)
18-OCT-20
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"Tiel and tie-2 define another class of putative receptor tyrosine
kinase genes expressed in early embryonic vascular system.";
Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Runting A.S., Stacker S.A., Wilks A.F.;
"Tie2, a putative protein tyrosine kinase from a new class of cell
surface receptor.";
Cowth Factors 9:99-105(1993).
                                                                                                                                                                                                                       50 SVCPC----ITFGQ-ISEILNKGTTSCGSRGALYCLLGLT-GLPSL-----YSCFYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Embryonic stem cells;
MEDLINE-93129253, PubMed-1282811;
HOTITA K., Yagi T., Kohura N., Tomooka Y., Ikawa Y., Aizawa S.;
"A_novel tyrosine kinase, hyk, expressed in murine embryonic stem
                                                                                                            82;
                                                                      8.8%; Score 81; DB 1; Length 300;
24.1%; Pred. No. 0.54;
.ive 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Res. Commun. 189:1747-1753(1992).
                                                                                                                                                 4 TVGYNLGLMKQPYVPPHYVSAPGTTTARWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CD-1; TISSUE-Embryonic heart; MEDLINE-93241731; Pubmed-8386827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Lung;
MEDLINE-94022374; Pubmed-8415706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE-Lung;
MEDLINE-94031116; PubMed-8217221;
                 33100 MW;
                                                                                                          46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      137 -----MGIG 140
                                                                                                                                                                                                                                                                                                                                                                                                         210 NAGLYDPAGVG 220
                 300 AA;
                                                                    Ouery Match
Best Local Similarity
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               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        Dumont D.J., Yamaguchi T.P., Conlon R.A., Rossant J., Breitman M.L.;
"Tek, a novel tyrosine kinase gene located on mouse chromosome 4, is
expressed in endothelial cells and their presumptive precursors.";
Oncogene 7:1471-1480(1992).
-!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
-i- SUBCELLIALIAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR ENDOTHELIAL CELLS.
MEDLINE=94244487; PubMed=8187650; Schnuerch H., Risau W.; "Expression of tie-2, a member of a novel family of receptor tyrosine kinases, in the endothelial cell lineage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; ECF-like domain; Transmembrane; Immunoglobulin domain; Clycoprotein; Phosphorylation; Wulligene family.

1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTABLE IN DAY 8.5 EMBRYOS. -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 2 IMMUNGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
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IG-LIKE C2-TYPE DOMAIN
EGF-LIKE 1.
EGF-LIKE 2.
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SMART; SM00060; FN3; 2.
SMART; SM0019; TYRKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0012; EGF 1; 3.
PROSITE; PS01186; EGF 2; 3.
                                                                                                                                                                                               SEQUENCE OF 822-1122 FROM N.A. STRAIN-CD-1; TISSUE=Embryonic heart; MEDLINE-9234855; PubMed=1630810; Vamaquchi T.P., Conlon.
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InterPro; IPR000561; EGF-like.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0019961; FN_III.
InterPro; IPR01245; Tyr_pkinase.
Pfam; PF00041; fn3; 3.
Pfam; PF00069; pkinase; 1.
PRINIS; PR00199; TYRKINASE.
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EMBL; X67553; CAA47857.1; --
EMBL; D13738; BAA02883.1; --
EMBL; S67051; AAB28663.1; --
PIR; S33142; S33142.
HSSP; P11662; IFGK.
                                                                                                                                                            Development 119:957-968(1993).
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PROSITE; PS00022; EGF_1; 17
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FIHSVPRHEVP -> LHPLSAPGMKYL (IN REF. 3).
                                                                                                                                                                                                                                                                                                                            221 SRPCTTCK--NNGVCH--EDTGECICPPGFMGRTCEKACEPHTFGRTCKERCSGPEGC-- 274
                                                                                                                                                                                                                                                                                                                                              74 RGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC----VDCLVHVFCEPCALCQEYRE 129
                                                                                                                                                                                                                                                                                           30; Gaps
                                                                                                                                                                                                                                                                                                            23 SAPGTTTARWSTGLCHCFDDPANCL-----VTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                        S -> C (IN REF. 1).
A -> G (IN REF. 1 AND 4).
MLLIAILGSAGMTCITV -> DATHSHPWVWNDFASPC
                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                .) (POTENTIAL)
                                                                            (POTENTIAL)
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MEDLINE-93049203; Pubmed-1425586;
Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,
                                                                                                                                                                                                   (IN REF. 3).
N -> NV (IN REF. 3).
R -> G (IN REF. 3).
AIANSTA -> CHRQOYS (IN REF. 3).
S -> P (IN REF. 3).
MW; F879623D103FFE96 CRC64;
                                                                                                                                                                                                                                                                        Ouery Match 8.8%; Score 81; DB 1; Length 1122; Best Local Similarity 24.1%; Pred. No. 2.1; Matches 32; Conservative 14; Mismatches 57; Indels
         DOMAIN 2.
                                                                                           (GLCNAC...) (GLCNAC...) (GLCNAC...) (GLCNAC...)
      IG-LIKE C2-TYPE DOMAIN FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3.
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                                                                N-LINKED GECN
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1122 AA; 125700 M
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EMBO J. 11:4519-4527(1992)
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SEQUENCE FROM N.A.
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REDITIRE—940.0571; Pubble-2022355; REDITIRE—940.0571; Pubble-2020.055; REDITIRE—940.055; REDITIRE—940.
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MEDLINE-98198405; PubMed-9531507;
Zhang H., Tan S.M., Lu J.;
"cDNA cloining reveals two mouse beta5 integrin transcripts distinct in cytoplasmic domains as a result of alternative splicing.";
Blochem. J. 331:631-637(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TISSUE=Liver;
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                                         SIMILARITY
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9; Mismatches
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SEQUENCE FROM N.A. (ISOFORM BETA-5A)
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Matches 34; Conservative
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PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
PROSITE; PS50025; LAM_G_DOMAIN; 5.
Callycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 22 POPTENWITAT
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LAMININ EGF-LIKE 13.
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      Feng X., Teitelbaum S.L., Quiroz M.E., Towler D.A., Ross F.P.; "Cloning of the murine beta5 integrin subunit promoter. Identification of a novel sequence mediating granulocyte-macrophage colony-stimulating factor-dependent repression of beta5 integrin gene
                                                                            ASSOCIATES WITH ALPHA V.

-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-5A (SHOWN HERE) AND BETA-5B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
-1- SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
                                    transcription..;
J. Blol. Chem. 274:1366-1374(1999)
J. Blol. Chem. 274:1366-1374(1999)
IF PUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
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MEDLINE-99098874; PubMed-9880508;
                                                                                                                                                                                                                                MGD: MGI:96614; Itgb5.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR002369; Integrin_B.
InterPro; IPR003659; PII.
InterPro; IPR002035; WWFA.
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EMBL; AF042255; AAC40109.1; -.
EMBL; AF022110; AAD08782.1; -.
HSSP: P04355; ZMRT.
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Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE PROFEIN TYROSINE KINASE TRANSMEMBRANE RECEPTOR.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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Eukaryota; Meta:oa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112)
TIEI OR TIE.
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Matches 32; Conservative
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214 GCGAGRWGPG---CTKECPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQE 270
                                                                  271 QCPGISGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPGHFGADCRLQCQ 320
                                  64 INKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVF
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
W; 3B42BE33678C58A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1.
                                                 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                              SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 77.5; DB 1; Length 1138;
24.6%; Pred. No. 4.8;
Ive 9; Mismatches 48; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE DOMAIN 2. FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3.
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SMART; SM00181; EGF; 2.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS500119; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00022; EGF_1; 3.
PROSITE; PS01186; EGF_2; 3.
                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; Fu_III.
InterPro; IPR003961; Fy_III.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000041; fin3; 3.
Pfam; PF00041; fin3; 3.
Pfam; PF000641; fig; 2.
Pfam; PF000641; fig; 2.
Pfam; PF000647; ig; 2.
Pfam; PF000647; ig; 2.
PRINTS; PR001099; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 63
161 161
503 503
596 596
1007 1007
1138 AA; 125089 M
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Best Local Similarity 24.69
                                  ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                  HSSP; P11362; 1FGK. MIM; 600222; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELORMENT OF THE RETURN.

-! SUBCELLULAR LOCATION: Extracellular (Potential).

-! SUBCELLULAR LOCATION: Extracellular (Potential).

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: A NATOSOMAL RECESSIVE CONDITION WHICH IS

CHARACTERIZED BY NIGHT BELINDESS FROM EARLY CHILDHOOD AND

PROGRESSIVE VISUAL FIELD LOSS. THERE IS GENERAL LOSS OF RETINAL

PROGRESSIVE VISUAL FIELD LOSS. THERE THAN AND PATIENTS EXPERIENCE

SEVERE VISUAL IMPAIRMENT BEFORE THE AGE OF TWENTY.

-! DISEASE: Defects in CRB1 are a cause of a form of Leber congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21303018; PubMed-11389483; den Hollander A.I., Heckenlively J.R., van den Born L.I., de Kok Y.J.M., van der Velde-Visser S.D., Kellner U., Jurklies B., van Schooneveld M.J., Blankenagel A., Rohrschneider K., Wissinger B., Cruysberg J.R.M., Deutman A.F., Brunner H.G., Apfelstedt-Sylla E., Hoyng C.B., Cremers F.P.M.;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS RP12 V-161; W-250; M-745; C-764; Y-948; Y-1014 AND P-1071.
TISSUB-Retina, and Fetal brain;
MEDLINE-99438399; PubMed-10508521;
den Hollander A.L., ten Brink J.B., de Kok Y.J.M., van Soest S., van den Born L.I., van Driel M.A., van de Pol D.J.R., Payne A.M., Bhattacharya S.S., Kellner U., Hoyng C.B., Westerveld A., Brunner H.G., Bleeker-Wagemakers E.M., Deutman A.F.,
Heckenlively J.R., Cremers F.P.M., Bergen A.A.B.;
"Mutations in a human homologue of drosophila crumbs cause retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Leber congenital amaurosis and retinitis pigmentosa with Coats-like exudative vasculopathy are associated with mutations in the crumbs homologue I (CRBI) gene.";
Am. J. Hum. Genet. 69:198-203(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.retina-international.com/sci-news/crblmut.htm".
                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME-Mutations of the CRB1 gene; NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-!- DATABASE: NAME=Mutations of the CRB1 gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT LCA ARG-1100, AND VARIANT RP ARG-1181.
                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                           Crumbs protein homolog 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 23:217-221(1999).
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amaurosis (LCA)
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                                                                                                                                                                                                                                          NCBI_TaxID=9606;
CRBH_HUMAN
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8;

48; Indels 41; Gaps

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GTTTARWSTGLCHCFDDPANCLVTSVC----PCI--

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24.68;

POTENTIAL

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           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EGF-LIKE 9.

LAMINING G-LIKE 1.

EGF-LIKE 10.

LAMINING G-LIKE 3.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

POTENTIAL.

POTENTIAL.
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CRUMBS PROTEIN HOMOLOG 1.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7.
EGF-LIKE 7.
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Length 1376; : Indels 52; Gaps	Score 77; DB 1; Pred. No. 6.5; 19; Mismatches 45	8.4%; larity 23.7%; Conservative	ו Similarity 36; Conserv	Query Match Best Local Si Matches 36;
E CRC64;	2 MW; F380DF2AA046A2F	AA; 15141;	1376	SEQUENCE
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	/FTId=VAR_011647. I -> R (IN LCA).	1100	1100	VARIANT
	L -> P (IN RP12).	1071	1071	ARIANT
	M -> T (IN RP12). /FTId=VAR 011646.	1041	1041	VARIANT
	/FTIG=VAR_011645.	74.0	η. Ε	VAKLANT
	/FTIG=VAR_011644.	. 0		EN 4 T C 4
	/FIIG=VAR_UIID45. R -> C (IN RP12).	764	764	VARIANT
	T -> M (IN RP12).	745	745	VARIANT
	C -> W (IN RP12). /FTId=VAR_011642.	250	250	VARIANT
	/FTIG-VAR_011641.	101	1	·
.) (POTENTIAL).	-LINKI	1273	1273	CARBOHYD
.) (POTENTIAL).	N-LINKED (GLCNAC	1265	1265	CARBOHYD
.) (POTENTIAL).	-LINKED (	1190	1190	CARBOHYD
.) (POTENTIAL).	-LINKED (	1000	1000	CARBOHYD
.) (POTENTIAL).	N-LINKED (GLCNAC	896	968	CARBOHYD
( POTENTIAL)	N-LINKED (GLCNAC.	871	871	CARBOHYD
.) (POTENTIAL).	-LINKED (	65 <i>/</i> 757	757	CARBOHYD
.) (POTENTIAL).	-LINKED (GLCNAC	561	561	ARBOHYD
.) (POTENTIAL).	-LINKED (	453 550	453 550	CARBOHYD
.) (POTENTIAL).	-LINKED	427	427	CARBOHYD
.) (POTENTIAL).	-LINKED (	322 418	322 418	CARBOHYD
.) (POTENTIAL).	_	313	313	CARBOHYD
.) (POTENTIAL).	-LINKED	215	215	ARBOHYD
.) (POTENTIAL).	N-LINKED (GLCNAC	4 4 2	4 4 4 2	CARBOHYD
.) (POTENTIAL).		30	30	ARBOHYD
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	POTENTIAL.	1312	1301	DISULFID
	POTENTIAL. POTENTIAL.	1283	1268	DISULFID
	POTENTIAL.	1274	1259	DISULFID
	POTENTIAL.	1249	1240	DISULFID
	POTENTIAL.	1229	1218	DISULFID
	POTENTIAL.	1211	1202	ISULFID
	POTENTIAL.	1191	1181	ISULFID
	POTENTIAL.	1174	1165	ISULFID
	POTENTIAL.	1154	1143	ISULFID
	POTENTIAL.	922	913	ISULFID
	POTENTIAL.	902	891	DISULFID
	POTENTIAL.	707	698	DISULFID

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MEDLINE—89280632; PubMed=2733383;
MEDLINE—89280632; PubMed=2733383;
AGOUNT MAGAYOSHI T., Fazio M., Peltonen J., Jaakkola S.,
Alsen D., Magayoshi T., Fazio M., Peltonen J., Jaakkola S.,
Alsen D., Sasaki T., Kulvaniemi H., Chu M.L., Deutzmann R.,
Thuman laminin: Cloning and sequence analysis of cDNAs encoding A, Bl
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RT and B2 chains, and expression of the corresponding genes in human
RT and B2 chains. The MEDIATE THE ATTACHMENT, MIGRATION, 6 ORGANIZATION OF
CELLS INTO TISSUES DURING EMBYONIC DEVELOPMENT BY INTERACTING
MITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CHELS THYO TISSUES DIRING EAKLOOFED MOLECULE
COMPRISING ONE LONG & THREE SHORY MITH GLOBULES AT EACH END
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORY ARMS WITH GLOBULES AT EACH END
CHAMININ-3 (S-LAMININ) AND
CHAMININ-3 (S-LAMININ) EXTRACELLULAR
CHAMININ-3 (S-LAMININ) 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPONENT).

DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
70 SCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQY-DLE------EAPC----- 109
                      154 SSPCQNGAVCQDGIDG----YSCFCVPGYQGRHCDLEVDECASDPCKNEATCLNEIGRYT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-2628 FROM N.A.
MEDLINE-91264789; PubMed=2049067;
Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P.,
Tryggvason K.;
"Pringayason K.;
"Pringay structure of the human laminin A chain. Limited expression in human tissues.";
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-9133420; PubMed-1714537;
Haaparanta_T., Uitto J., Ruoslahti E., Engvall E.;
"Molecular cloning of the cDNA encoding human laminin A chain.";
Matrix 11:151-160(1991).
                                                                                                                                                                                                IMA1_HUMAN STANDARD, PRT; 3075 AA. P25391, PL AV-1992 (Rel. 22, Created) Ol-MAY-1992 (Rel. 22, Last sequence update) Ol-MAR-2002 (Rel. 41, Last annotation update) Laminin alpha-1 chain precursor (Laminin A chain).
                                                                      110 ------VDCLVHV---FCEPC---ALCQE 126
                                                                                             210 CICPHNYSGVNCELEIDECWSQPCLNGATCQD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 276:369-379(1991).
                                                                                                                                                                                                                                                                                                               LAMA1 OR LAMA.
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CC or send an email to licensetiab-sib.ch).

DR REAL SASSII (AASA 118.1): -

DR REAL SASSII (AASA 118.1): -

DR REAL SASSII (AASA 118.1): -

DR RICE SASSII (AASA 118.1): -

DR REAL SASSII (A
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tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINATLY EXPRESSED IN ENDOTHELIAL CELLS
AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILLCAL VEIN
ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS
CHARACTERIZED BY DILATED, SERPICINOUS CHANNELS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97134665; PubMed-8980225; Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J., Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C., Mulliken J.B., Olse B.R.;
                             | :|:|:|:|:|:
-----GCTDEGQCHCVPGVAG-KRCDRCAH-----GFYAYQDGSCTPCDCPHTQNTCD 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS VACMI TRP-849 AND SER-897.

VARIANTS VACMI TRP-849 AND SER-897.

VARIANTS VACMI TRP-849 AND SER-897.

VARIANTS WOMEN T. S. TOOTICS C. D., Cha E.H., Prieto V.G., Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A., Speer M.C., Peters K.G., Marchuk D.A.;

Speer M.C., Peters K.G., Marchuk D.A.;

Hum. Mol. Genet. 8:1279-1289(1999).

-1- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR FOR ANGIOPOLETIN I. IT MARY CONSTITUTE THE EARLIEST MAMMALIAN ENDOTHELIAL CELL INREGE MARKER. PROBABLY RECULATES ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
                63 ILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDC-LVHV--FCE 119
                                                                                                                                                                                                                                                                                                           2iegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
"Molecular clohing and characterization of a novel receptor protein
tyrosine kinase from human placenta.";
Oncogene 8:663-670(1993).
                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TIE)
TIEK) (Tunica interna endothelial cell kinase).
                                                                                                                                                                                                                                                                                                                                                                                                              "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2."; Cell 87:1181-1190(1996).
                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
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                                                         -----CALCQEYRELKNRGFDMGIGWQA 143
                                                                                                                              PRT; 1124 AA
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MEDLINE=93173509; PubMed=8382358;
                                                                                                                              STANDARD;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                      Repeat; EGF-11ke domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family; Disease mutation. SIGNAL
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8.1%; Score 75; DB 1; Length 1124;
Best Local Similarity 23.3%; Pred. No. 8.4;
Matches 30; Conservative 15; Mismatches 52; Indels
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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ATP (BY SIMILARITY).
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InterPro; IPR00079; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0001961; FN_III.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000041; ff3; 3.
Pfam; PF000141; ff3; 3.
Pfam; PF00069; PKINASE.
SWART; SW00181; EGF; 2.
SWART; SW00001; EGF_11ke; 1.
SWART; SW00001; EGF_11ke; 1.
SWART; SW00001; EGF_11ke; 1.
PR051TE; PS00107; PROTEIN_KINASE_TYR; 1.
PR051TE; PS00107; PROTEIN_KINASE_TYR; 1.
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EGF-LIKE 2.
EGF-LIKE 3.
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                                                                                  EMBL; L06139; AAA61139.1; -. HSSP; P11362; 1FGK.
MIM; 60021; -. MIM; 600195; -.
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00022; EGF_1; 3
PROSITE; PS01186; EGF_2; 3
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Gaps

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29 TARWSTGLCHCFDDPANCL-----VTSVCPCITFGQISEILNKGTTSCGSRGALYC 79

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
80 LLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVFCEPCALCQEYRELKNR 133
                        -----LPDDPYGCSCATGWKG-LQCNEA-CHPGFYGPDCKLRCSCNNGEMCDRF----Q 327
                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

SIGNAL 1 19 POTENTIAL.
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EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kraus G.K., Talbott R., Leavitt M., Luznick L., Schmidt A., Badel P., Bartz C., Morton W., Wong-Stal F., Looney D.J.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=73484;
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InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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Perfect score:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Q9fgn2 arabidopsis
P94032 arabidopsis
Q9gqe8 arabidopsis
Q9fg0 oryza sativ
Q9fd92 oryza sativ
Q9m5d4 chlamydomon
Q9j148 mus musculu
Q9nzii homo sapien
Q9ej4 homo sapien
                                                                                                                                     096815 arabidopsis
096529 arabidopsis
096771 mus musculu
099405 homo sapien
022563 arabidopsis
094314 oryza sativ
095646 leishmania
094791 drosophila
097711 drosophila
097711 masculu
096731 podocoryne
09631 podococyne
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09rlkl rattus norv
09rlk0 rattus norv
09wts5 mus musculu
09rlk2 rattus norv
09caj7 arabidopsis
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SEQUENCE FROM N.A.
Frary A., Grandillo S., van der Knaap E.,
Cong B., Liu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;
"fw2.2: a quantitative trait locus key to the evolution of tomato fruit size.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQ1 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYPIVGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon pennellii (Tomato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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EMBL; AF261775; AAF74287.1; -.
SEQUENCE 163 AA; 18062 MW; 0628795F184B4869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAGMTR 163
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ilarity 100.0%; Pred. No. 1.3e-98;
Conservative 0; Mismatches 0;
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Q943N4
Q15846
Q24550
Q9VY11
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Q9FN61
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Best Local Similarity
Matches 163; Conserv
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01-OCT-2000
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                                                                                                                                                                                                 1 MYPTVGYNLGLMKQPYVPPH......NMDRQSRGVTMPPYHAGMTR 163
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                     July 15, 2002, 06:46:57; search time (without 1022.043
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                                                                                                                                                                                                                                                                                562222 segs, 172994929 residues
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                                                                             protein search, using sw model
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09LKV7
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09LQU2
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Q9FPE1
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_invertebrate:*
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Maximum Match 100%
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Gaps

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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Rhan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Chon L., Choway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Leaz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Lee J., Leaz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., A. Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Leaglis A., Ecker J., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

RIML: AC006917 ARF92351;
RIML: ARCOGOGIS. Asx_hydroxyl.
RIML: ACCOMMINIATION REPROSITE: PS00010; ASX_HYDROXYL, UNKNOWN_1.
                                                                        Johnson-Hopson C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskala V.S., Schwartz J.R., Liu A., Liu K., Vaysberg M., Sakano H.,
Cha J., Gnoralez A., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
Submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO08075; AAA049981.1; -.
EMBL; ACO08075; AAA049981.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GTTSCGSRGALYCLL-GLTGL--PSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 ALYCLLG-LTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 YVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 NLGLMKQPYVPPHYVSAPGTTTAR-WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK 66
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 433; DB 10;
Pred. No. 3.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.8%; Score 403.5; DB
llarity 48.5%; Pred. No. 9e-39;
Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 AA
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
47.0%; Score 433; DB
Best Local Similarity 51.0%; Pred. No. 3.3e
Matches 78; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 FDMGIGWQANMDRQSR--GVTM--PPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 YDMSLGWAGNVERQQNQGGVAMGAPVFQGGMTR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q9SX24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SEILNKGTTSCGSRGALYCLLGLFGLFSLYSCFYRSKWRGQYDLEEAPCVDCLVHVFCEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.,
"Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQI 60
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Frary A., Nesbitt T.Clint, Frary A., Grandillo S., van der Knaap E.

Copp B., Llu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;

"fw2.2: a quantitative trait locus key to the evolution of tomato
fruit size.";
                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF261774; AAF74286.1; -. SEQUENCE 163 AA; 18061 MW; AA46EA140B7A8803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAGMTR 163
                                                                                                               Q9LKV7;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.6%; Score 899; DB 10;
98.2%; Pred. No. 4.6e-96;
iive 0; Mismatches 3;
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                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                           PRELIMINARY;
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Submitted (FEB-1999)
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Matches 160;
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                                                                                           Q9LKV7
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Q9LQU4
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                                                                   Q9LKV7
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224 AA;
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hes 74; Conserv
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                                   01-DEC-2001
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   01-MAY-1999
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                                                                     PGPS/D12.
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Matches
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Con L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaotoria A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006917; AAF79233.1; -. SEQUENCE 151 AA: 16503 MW; 7D17F5B8CA5E9368 CRC64;
54 GSTSCGVSGAMYMIIFMLTGYGGSSLYSCFYRTKLRAQYNLKERPCCDCCVHFCCEPCAL 113
                                                                                                                                                                                                                                                                                                                                                                            Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskala I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskala V., Yu G., Boavis R.W., Federsphel N.A., Theologis A., Ecker J.R.; "Genomic sequence for Arabidopsis thallana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 RGALYCLLGL-TGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicales; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.8%; Score 403; DB 10; Length 151; Best Local Similarity 48.4%; Pred. No. 9.6e-39; Matches 75; Conservative 21; Mismatches 47; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                   124 CQEYRELK-NRGFDMGIGWQANMDRQSR----GVTMPPYHAGMTR 163
                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 RGFDMGIGWQANMDRQSR--GVTM--PPYHAGMTR 163
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092TM8;
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Q9LQU2
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SEQUENCE FROM N.A.
TISSUB-GERMINATING PETUNIA POLLEN TREATED WITH KAEMPFEROL;
MEDLINE-20317212; PubMed-10859200;
GUYON V.N., Astwood J.D., Ganner E.C., Dunker A.K., Taylor L.P.;
Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia.";
Plant Physiol. 123:699-710(2000).
EMBL, AF049928; AAD02254-1;
SEQUENCE 145 AA; 16302 MW; 9835DB8F584E9344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 SGTVYLLVYLVTSGFGCCWYSCFYRSKLRNQYYLDEKPCSDLCTHCCCEYCALCOEYREL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 RGALYCLLGL--TGLPSL-YSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYREL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MYPTVGYNLGLMKQP-YVP-------PHYVSAPG---TTTARWSTGLCHC 39
                                                                                                                                                            Petunia hybrida (Petunia).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
NCBI_TaxID-4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F27J15.18.
                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 378; DB 10;
47.7%; Pred. No. 7.1e-36;
tive 19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 KNRGFDMGIGWQANMD--RQSRGVTMPPYHAGMTR 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana (Mouse-ear cress).
         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24875 MW;
(TrEMBLrel. 10, (TrEMBLrel. 10, I (TrEMBLrel. 19, I
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41.8%;
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Best Local Similarity 41.83
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
             core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 YSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 FSCTYRTKIRSKFGLPESPTSDCVTHFFCECCALCQEHRELKTRGLDPSIGWSGNWQR-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGLPSL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequen features of the regions of 4,504,864 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 3. I. Seque
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s: ;
                                                                                                                           Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Kaneko T., Kato T., Asamizu E., Tabata to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                            4B9AB72DCAF5A386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F2CF624443039B0E CRC64;
               Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0c7-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MYF24.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 319.5; DB 10; 39.9%; Pred. No. 5.4e-29; iive 31; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 347; DB 10;
; Pred. No. 2.5e-32;
21; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                    MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                 clones.";
DNA Res. 7:131-135(2000).
EMBL; AB026658; BAB01113.1; -.
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EMBL; AB02658; BAB01111.1; -.
SEQUENCE 184 AA; 20103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   37.78;
48.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.7
Best Local Similarity 39.9
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                       SEQUENCE FROM N.A. STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ---TMAP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COLUMBIA;
Sato S., Nakamura
                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                     STRAIN-COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura Y.;
                                                                                                                                                                                                                                     Nakamura Y.;
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Q9LS45;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MYE24.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 CFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQSRG 151
                                                                                                                           99 RGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQSRG----VTM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
               95
                                                   40 FDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGLPSLYSCFYRSKM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana chromosome 3. I. Seque features of the regions of 4,504,864 bp covered by sixty Pl and TAC clones.":
:|| | |::|| || 39 IYPNNG---GVVNQPNQVPMRPGPPTYINQSATFNQPYGVSMAGPVHTQPSNWTSGLFDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -.
?: 9D07D3F21AA0BF84 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, Pl CLONE: MYF24.
Arabidopgis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.9%; Score 358.5; DB 10; 49.6%; Pred. No. 1.7e-33;
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                                                                                                                                                                                                                                                                                                                             184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Mismatches
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                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE-20277480; Pubmed-10819329;
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AB026658; BAB01112.1; -.
NCE 184 AA; 20150 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 VTMPP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 VMSPP 177
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01-0CT-2000 (7
01-0CT-2000 (7
01-0CT-2000 (7
01-0CT-2000 (7
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                                                                                                                                                                                                                              PP 217
                                                                                                                                                                                                   155 PP 156
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONA Res.
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Matches 6
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Q9LS44;
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09SX26;
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Q9SDC9
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01-MAR-2001 (TEMBLEEL: 16, Last annotation update)
01-MAR-2001 (Marcheel: 16, Last annotation update)
01-MAR-2001 (TEMBLEER: 16, Last annotation update)
01-MAR-2001 (TEMBLEEL: 16, Last annotation update)
01-MAR-2001 (TEMBLEER: 16, Last annotation update)
01-MAR-2
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STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Malti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                          S DEGATPCATAGLLYGALFFIGASFVYSYMFRARIRKKKGLPDAPAPDWITHLYCMPFALC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 QISEILNKGTTSCGSRGALYCLL----GLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 PVTGIPVG-MFYPAPPMERVVSCRMAPAAGGA-WTTALCDCADDCNTCCMACWCPCIPVG 76
                 64
                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Sukaryota, Vilidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                 VGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEIL
                                                         25 VSHNGGIGKPANIPTGIPVNYQQTQNQWSSQLFDCMNDSENAVITLIAPCVTFGQIAEIV
                                                                                                    NKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood T., Yu Y., Soderlund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 299.5; DB 10; Length
Pred. No. 9.6e-27;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing R.A., Filsch D., Presting G., Wood T., Yu Y., Soder Kim H., Rambo T., Henry D., Simmons J.; Rice Genomic Sequence."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ACO'9685; AAR5282.1; SEQUENCE 161 AA; 17230 MW; 6966EBB537413153 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AA
                                                                                                                                                                                    125 QEYRELKNRGFDMGIGWQANMDR-QSRGVTMPP 156
                                                                                                                                                                                                             161
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 VHVFCEPCALCQEYRELKNRGFDMGIG 140
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                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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42.9%;
                                                                                                                                                                                                                                                                                                                                                         Q94L14;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
UNKNOWN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 63; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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Q9M815
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094LI4
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STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskaia V.S., Schwartz J.R., Liu A., Liu K., Vaysberg M., Sakano H.,
Che J.M., Li J., Gonzalez A., Liu A., Liu K., Waysberg M., Sakano H.,
Chio E., Choi J., Altafi H., Araijo R., Brooks S.,
Buehler E., Chao Q., Coon L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
"The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.";
Submitted (AdC.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC008075; AAD49982.1.
EMBL, AC008075; RAN, E468A0F52F9F9A71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 KHLDFGGNAACMNAGLIHIALGFIGCSWLYAFPNRSRLREHFALPEEPCRDFLVHLFCTP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 RGALYCLLGLFGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVPPHYVSAPGTTTA--RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                                                                                                                                                                   35 FAPPNYQQANVNLSVGRPWSTGLFDCQADQANAVLTTIVPCVTFGQIAEVMDEGEMTCPL 94
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thatlana chromosome 1 BAC F915 genomic sequence."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC022354; AAF29406.2; -
                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 270.5; DB 10; Length 174; Pred. No. 2.4e-23; 20; Mismatches 61; Indels 21;
                                                                                                                                                                                                                               Length 190;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                            21179 MW; 9708EF167B0031C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHA-GMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         31.3%; Score 288; DB 10;
llarity 39.9%; Pred. No. 2.5e-25;
Conservative 27; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | | :|| | :|| ELKIRNLDPSLGWNGILAQGQGGYEREA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKNRGFDMGIGW-----QANMDRQS 149
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190 AA; 2
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                                                                                                                    Hypothetical
                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 59;
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Best Local S
Matches 62
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A Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk K., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.; Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.;
Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 VTSVCPCITFGQISEILNKGTT--SCGSRGALYCLL------GLT-GLP----SLYS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LINKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK---G 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 147;
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
SASAKI T., Matsumcto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000969; BAA88537.1; --
SEQUENCE 147 AA; 15696 MW; 950D30E2A111508B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FPE1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
HYPOTHETICAL 26, 6 KDA PROTEIN (FRAGMENT).
114P1.19/AT2G45010.
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 CFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.0%; Score 193; DB 10;
39.2%; Pred. No. 1.8e-14;
tive 17; Mismatches 29;
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147 AA.
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                                                    Created)
PRT;
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                                            01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, ESTS AU082078(C53435).
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PRELIMINARY;
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                                                                                                                                                          Oryza sativa (Rice)
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Best Local Similarity
Matches 40; Conserv
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Search completed: July 15, 2002, 06:50:43 Job time: 226 sec \_

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AAG36900
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Pathogen response
Arabidopsis thalia
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2. \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1980.DAT:*
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17. \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1991.DAT:*
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595.952 Million cell updates/sec
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                                                                                      July 15, 2002, 06:46:37 ; Search time 30.38 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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AAG16620
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AAG10514
AAG14719
AAG46457

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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921
1 MYPTVGYNLGLMKQI
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length: 2000000000
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Match
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331.4
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06	79	133	133	9/	70	198	198	244	244	106	240	241	240	241	242	242	242	169	169	115	115	115	120	115	130	130	357	357	384	384	421	421	188	
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231.5	226	211	211	207	194	193	193	193	193	170	166	166	164	164	164	164	164	140	138	134	134	134	134	132	128	128	123	123	123	123	123		117.5	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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                                                                                                                                                                                                                                          Gaps
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52.0%; Pred. No. 2.5e-37;
tive 20; Mismatches 40;
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                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                              Query Match 43.8%; Score 403.5; DB 21; Length 160; Best Local Similarity 48.5%; Pred. No. 5.2e-35; Matches 80; Conservative 27; Mismatches 41; Indels 17;
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                                                                                                                                                                                                                                                                                                                124 CQEYRELK-NRGFDMGIGWQANMDRQSR----GVTMPPYHAGMTR 163
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PR 21-ULL 1999 9905-0144684.

PR 22-ULL 1999 9905-0145688.

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PR 02-MC-1999 9905-014514.

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48.5%; Pred. No. 5.7e-35;
ive 27; Mismatches 41; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                             Query Match 43.8%; Score 403; DB 21; Length 151; Best Local Similarity 48.4%; Pred. No. 5.5e-35; Matches 75; Conservative 21; Mismatches 47; Indels 12;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                               42 DPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGL--PSLYSCFYRSKM 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 8869.
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990S - 0159293 . 990S - 0159294 . 990S - 0159294 . 990S - 0159329 . 990S - 0159330 . 990S - 0159330 . 990S - 0159330 . 990S - 015928 .
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74 RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
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                                                                                                                                                                                                                                                                                                      Length 194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    31.4%; Score 289; DB 21; 38.1%; Pred. No. 9.9e-23;
                                                                                                                                                                                                                                                                                                                        29; Mismatches
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  4;
                                                                                                               This is the amino acid sequence of LSD1-interacting protein K of Arabidopsis thaliana. LSD1 interacting genes (see AAV66755-67) were isolated from a yeast gene expression library constructed in plasmid pGd4-5 using RNA from Arabidopsis leaves infected with Esplasmid pGd4-5 using RNA from Arabidopsis leaves infected with and long open reading frames (see AAV66750-51) as bait. LSD1 (see AAV67356-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Since the inactivation of LSD1 by mutation leads to enhanced disease resistance, LSD1 partner proteins represent novel targets for engineering plants includes all proteins (see AAW72384-96) that interact with the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                          74 RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                 44; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                     16 YVPPHYVSAPGITIA--RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                   New isolated Arabidopsis genes - useful for producing transgenic plants which show resistance to cell death caused by pathogens or herbicides.
                                                                                                                                                                                                                                                                                                          ch 31.3%; Score 288; DB 19; Length 188; I Similarity 39.9%; Pred. No. 1.2e-22; 59; Conservative 27; Mismatches 44; Indels 18
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 Richberg MH;
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elkirnldpslgwngilaggggggyerea 176
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 Epple PM,
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                                                                                            Claim 46; Page 63; 88pp; English.
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990S-0123180.
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Dangl JL, Dietrich RA,
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                   WPI; 1998-531501/45.
N-PSDB; AAV66762.
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Best Local S:
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R 19-JUL-1999, 9018-0144331.

R 19-JUL-1999, 9018-0144331.

R 20-JUL-1999, 9018-0144331.

R 20-JUL-1999, 9018-0144332.

R 20-JUL-1999, 9018-015108.

R 20-JUL-1999, 9018-015109.

R 20-JU
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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.8e-22;
es 37; Indels 45;
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                                                                                                                                                                                                                                                                                                                                                                                                               30.5%; Score 280.5;
llarity 37.4%; Pred. No. 7.8e
Conservative 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 50045.
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les 61; Conservative
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 45.5%; Pred. No. 5.2e-17;
Matches 45; Conservative 11; Mismatches 24
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PR 11-AUG-1999; 9908-0149177.

PR 11-AUG-1999; 9908-0149177.

PR 27-AUG-1999; 9908-0151086.

PR 28-EEP-1999; 9908-0151086.

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